

(19)



Europäisches Patentamt

European Patent Office

Office européen des brevets



(11)

EP 0 785 999 B1

(12)

EUROPEAN PATENT SPECIFICATION

(45) Date of publication and mention
of the grant of the patent:

12.05.2004 Bulletin 2004/20

(21) Application number: **95929671.6**

(22) Date of filing: **30.08.1995**

(51) Int Cl.7: **C12N 15/82, A01H 5/00**

(86) International application number:
PCT/AU1995/000552

(87) International publication number:
WO 1996/006932 (07.03.1996 Gazette 1996/11)

(54) **PLANT TRANSCRIPTION REGULATORS FROM CIRCOVIRUS**

PFLANZENTRASKRIPTIONSREGULATOR VON CIRCOVIRUS

REGULATEURS DE TRANSCRIPTION VEGETALE ISSUS DE CIRCOVIRUS

(84) Designated Contracting States:
AT BE CH DE DK ES FR GB GR IE IT LI NL PT SE

(30) Priority: **30.08.1994 AU PM777094**
07.11.1994 AU PM928194

(43) Date of publication of application:
30.07.1997 Bulletin 1997/31

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(56) References cited:
WO-A-96/38554 WO-A-96/38564
DE-C- 4 306 832

- **YEH, H.-H., ET AL.: "Genome characterization
and identification of viral-associated dsDNA
component of Banana bunchy top virus"
VIROLOGY, vol. 198, February 1994, pages
645-652, XP002058107**
- **WU, R.Y., ET AL.: "Banana bunchy top virus
(BBTV DNA I) VI and C1-C3 genes, complete
cds's" EMBL SEQUENCE DATABASE
ACCESSION NO. L32166, 11 August 1994,
XP002058108**
- **WU, R.Y., ET AL.: "Banana bunchy top virus
(BBTV DNA II) V1,V2,C1 and C2 genes, complete
cds's" EMBL SEQUENCE DATABASE
ACCESSION NO. L32167, XP002058109**
- **VIROLOGY, Volume 207, pages 354-361, (1995),
P. BOEVINK et al., "Sequence of Subterranean
Clover Stunt Virus DNA: Affinities with
Geminivirus".**
- **JOURNAL OF GENERAL VIROLOGY, (1995),
Volume 76, pages 475-479, KATUL LINA et al.,
"Sequence Analysis of a Faba Bean Necrotic
Yellow Virus DNA Component Containing a
Putative Replicase Gene".**
- **JOURNAL OF GENERAL VIROLOGY, (1994),
Volume 75, pages 3541-3546, KARAN MIRKO et
al., "Evidence for Two Groups of Banana Bunchy
Top Virus Isolates".**

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EP 0 785 999 B1

- PHYTOPATHOLOGY, Volume 84, No. 9, issued 1994, pages 952-958, WU R.Y. et al., "Nucleotide Sequences of Two Circular Single-Stranded DNAs Associated With Banana Bunchy Top Virus".
- PHYTOPATHOLOGY, Volume 85, No. 3, (1995), XIE W.S. and HU J.S., "Molecular Cloning Sequence Analysis and Detection of Banana Bunchy Top Virus in Hawii", page 344.
- VIRUS RESEARCH, Volume 27, (1993), pages 161-171, CHU PAUL W.G. et al., "Putative Full-Length Clones of the Genomic DNA Segments of Subterranean Clover Stunt Virus and Identification of the Segment Coding for the Viral Coat Protein".
- VIRUS RESEARCH, Volume 27, (1993), pages 173-183, CHU PAUL W.G. et al., "Replication of Subterranean Clover Stunt Virus in Pear and Subterranean Clover Protoplasts".

Description

[0001] The present invention relates generally to a novel range of transcription regulators and transcription regulator-like sequences operable in plants. More particularly, the present invention is directed to transcription regulators and transcription regulator-like sequences of viral origin and, even more particularly, of circovirus origin. The transcription regulators and transcription regulator-like sequences of the instant invention are useful in genetic engineering of plants and in particular leguminous plants such as to facilitate or control expression of foreign genes. The transcription regulators and transcription regulator-like sequences of the present invention are also useful in facilitating different levels of expression in different plant tissue types.

[0002] Bibliographic details of the publications referred by author in this specification are collected at the end of the description. Sequence Identity Numbers (SEQ ID Nos.) for the nucleotide sequences referred to in the specification are defined following the bibliography.

[0003] Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

[0004] Transcription regulators are molecules, and generally nucleotide-based molecules, which facilitate and modulate expression of genetic sequences at the level of transcription. Transcription regulators include promoters and termination and polyadenylation sequences amongst other effectors and facilitators of transcription.

[0005] Promoters are specific nucleotide sequences to which RNA polymerase binds to initiate RNA synthesis in cells. They contain the start site for RNA synthesis and the genetic signals to initiate polymerase mediated RNA synthesis. In addition, sequence specific DNA-binding proteins are presumed either to inhibit or to stimulate the initiation of RNA synthesis by binding next to the promoter and affecting the binding of the polymerase to the promoter. Terminator sequences refer to termination and polyadenylation sequences and are required for transcription of functional mRNAs. Termination sequences are located downstream (i.e. at the 3' end) of a gene and are recognized by RNA polymerase as a signal to stop synthesizing mRNA. Polyadenylation sequences are signals required for polyadenylation of eukaryotic mRNA molecules following transcription.

[0006] A viral promoter widely used to facilitate foreign gene expression in plants is the cauliflower mosaic virus (CaMV) 35S promoter (Odell *et al.* 1985), which is derived from a double-stranded DNA plant virus. The use of this promoter in plants and plant cells is well documented (Benfey and Chua, 1990; Higgins and Spencer, 1991). However, despite the apparent usefulness of this promoter, it is not functional in all plants and is particularly poorly operable in leguminous plants. There is a need, therefore, to identify other promoters, such as of viral origin, which are operable in plants and particularly leguminous plants. There is also a need to modulate levels of expression of genes and other genetic sequences within plant cells.

[0007] Accordingly, one aspect of the present invention is directed to a genetic construct comprising a circovirus promoter or promoter-like sequence and which is operable in a plant cell.

[0008] In a related aspect of the present invention, there is provided a genetic construct comprising a circovirus promoter or promoter-like sequence and a termination and/or polyadenylation sequence, which sequences are operable in a plant cell.

[0009] A circovirus is a non-geminated single stranded (ss) DNA plant virus (Table 1), distinct from caulimoviruses which have a double stranded genome, and geminiviruses, the only other known ssDNA plant viruses, which have geminated particles (Chu *et al.*, 1994). As used herein, the circovirus group is considered to include subterranean clover stunt virus (SCSV) (Chu and Helms, 1988), coconut foliar decay virus (CFDV) (Rohde *et al.* 1990), banana bunchy top virus (BBTV) (Thomas and Dietzgen, 1991; Harding *et al.* 1991; 1993; Burns *et al.* 1993) and milk-vetch dwarf virus (MDV) (Isogai *et al.* 1992; Sano *et al.* 1993) and faba bean necrotic yellows virus (FBNYV) (Katul *et al.*, 1993).

[0010] In a particularly preferred embodiment, the circovirus contemplated for use in accordance with the present invention comprises more than two DNA components or segments.

[0011] The present invention is particularly directed and hereinafter described with reference to subterranean clover stunt virus (hereinafter abbreviated to "SCSV") as a representative of the circovirus group. This is done, however, with the understanding that reference to SCSV includes reference to all other suitable members of the circovirus group to which the instant invention extends. Preferred members of the circovirus group such as SCSV comprise more than two DNA components or segments. Reference hereinafter to "SCSV" also includes and extends to all naturally occurring or artificially induced mutants, derivatives, parts, fragments, homologues or analogues of the virus which still retain at least one suitable promoter and/or termination and/or polyadenylation sequences.

[0012] Accordingly, a particularly preferred embodiment of the present invention contemplates a genetic construct comprising an SCSV promoter or promoter-like sequence and which is operable in a plant cell.

[0013] A related aspect of the present invention is directed to a genetic construct comprising an SCSV promoter or promoter-like sequence and a termination and/or polyadenylation sequence, which sequences are operable in a plant

cell.

[0014] The term "genetic construct" is used in its broadest sense to include any recombinant nucleic acid molecule such as an isolated nucleic acid molecule, vector, expression vector or binary vector. It may comprise solely the circovirus promoter or may contain one or more promoters in association with regulatory and/or reporter sequences.

[0015] The genetic construct may be double or single stranded DNA, in linear or covalently closed circular form. As stated above, it may comprise only the promoter or promoter-like sequence or may carry other heterologous or homologous transcription regulator sequences and/or heterologous structural gene sequences including promoters associated with SCSV. By "homologous" is meant a gene sequence naturally associated with the SCSV promoter. "Heterologous" means a "foreign" gene relative to the promoter or a gene not otherwise normally associated with the SCSV promoter. In a preferred embodiment, the foreign gene is also foreign to SCSV. Examples of foreign genes include genes which facilitate resistance to insects or other pest infestation, enhance resistance to insecticides or herbicides, promote frost resistance, alter flower or petal colour, decrease the rate of senescence, especially in cut flowers, increase or enhance levels of certain proteins and/or ribozymes. More particularly, the foreign genes include:

- a) a resistance gene against plant viruses, bacteria, fungi, nematode and other pathogens;
- b) a plant virus resistance gene including a synthetic gene from and against alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato viruses x, y, s, m and a, cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;
- c) a gene to improve nutritional value of plants such as sunflower high sulphur gene SF8;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene including BT toxin gene and proteinase inhibitor gene from *Nicotiana glauca*;
- h) a selectable marker gene such as those conferring resistance to kanamycin, phosphinothricin, spectinomycin and hygromycin;
- i) a reporter gene such as GUS, CAT and pigment genes;
- j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

[0016] The present invention further contemplates a genetic construct comprising two heterologous genes operably linked to the same or different circovirus promoters operable in a plant cell. Preferably the promoter or different promoters are from a circovirus with a genome comprising more than two components or segments. Most preferably the promoter or different promoters are from SCSV and in particular are selected from segments 1 to 7 of SCSV as defined by SEQ ID NOs. 1 to 7. (See below). The genetic constructs may also comprise a termination or polyadenylation sequence operably linked to one or both of the heterologous genes. In one embodiment, the termination and/or polyadenylation sequence is the same for each gene. In an alternative embodiment the termination and/or polyadenylation sequence is different for each gene. Most preferably the termination and polyadenylation sequence is selected from segments 1 to 7 of SCSV as defined by SEQ ID NOs. 1 to 7 (See below). In yet another embodiment at least one termination and polyadenylation sequence is from the MeA 3 gene of *Flaveria bidentis* (see below).

[0017] The term "transcription regulator" is used in its broadest sense to include promoters, termination and polyadenylation sequences and other effectors and facilitators of transcription of genetic sequences. As with promoters contemplated by the present invention, the termination and polyadenylation sequences may be of SCSV origin and may be naturally associated with a corresponding promoter from SCSV or may be associated with another promoter of SCSV. Alternatively, the termination and/or polyadenylation sequences may be derived from non-SCSV sources. A particularly preferred terminator comprises the 3' nucleotide sequence of the MeA3 gene of *Flaveria bidentis* which codes for an NADP-malic enzyme of C4 photosynthesis (Hatch, 1987). The nucleotide sequence of the terminator region of the MeA gene is shown in Figure 15. The combination of an SCSV promoter with, for example, the *F. bidentis* MeA gene terminator sequence results in a high level of expression especially in monocotyledonous plants relative to constructs without the terminator sequence.

[0018] The foreign gene may also be in the antisense orientation so as to facilitate reduced levels of endogenous plant gene products. In this regard, "gene" may be ten base pairs in length, tens of base pairs in length, hundreds of base pairs in length or a full length or near full length gene but in a reverse orientation relative the promoter. The foreign gene may also be placed in the "sense" orientation for co-suppression of a target gene.

[0019] According to another aspect of the present invention, there is provided a genetic construct comprising an SCSV promoter or promoter-like sequence operable in a plant cell and at least one restriction endonuclease site downstream of said promoter to facilitate insertion of a heterologous gene such that said gene is operably linked to said promoter. In an alternative embodiment, the genetic construct comprises an SCSV promoter or promoter-like sequence operable in a plant cell and a heterologous gene operably linked to said promoter. In both embodiments, the term

"gene" includes those directing the synthesis of oligonucleotides such as those useful in antisense techniques as well as ribozymes.

[0020] In still a further embodiment of the present invention, there is contemplated a genetic construct comprising an SCSV promoter or promoter-like sequence operable in a plant cell and at least one restriction endonuclease site downstream of said promoter to facilitate insertion of a heterologous gene such that said gene is operably linked to said promoter and a termination and/or polyadenylation sequence positioned such that same sequence is at the 3' end relative to said heterologous gene to facilitate expression of said heterologous gene. Preferably, the termination sequence is from SCSV. Alternatively, the terminator sequence is from the *F. bidentis* MeA3 gene.

[0021] Plants contemplated by the present invention include both monocotyledonous and dicotyledonous species. The present invention also extends to leguminous and non-leguminous plants although leguminous plants are preferred.

[0022] The SCSV genome comprises at least seven distinct circular ssDNA components described as segments 1-7. The size of these segments range from about 988 to about 1022 nucleotides. Each of the seven DNA components of SCSV contains one major open reading frame of the viral sense and a non-coding region of various lengths containing a conserved potential stem and loop structure (Figures 1 and 2; Table 2). Each transcription unit contains a typical TATA box and a polyadenylation signal for start and end of transcription, respectively (Figure 2, Table 2).

[0023] Because the DNAs are circular, the sequences in the non-coding regions comprise the promoters and the terminator signals which vary with different DNA components (Table 2). The TATA boxes and the stem-loops of the two replicase-associated protein genes in segments 2 and 6 are quite different from those of the other genes. In contrast, the stem-loops and TATA boxes are the same in segments 1, 3, 4, 5 and 7. All the DNAs, except those of segments 2 and 6, also share a common sequence (known as the common region) in the non-coding region (Figures 1 and 2).

[0024] The present invention, therefore, extends to each of the seven promoters and to termination and polyadenylation sequences on segments 1-7 of SCSV. The nucleotide sequences of segments 1-7 are shown in Figure 6 and are defined in SEQ ID NOs. 1-7, respectively.

[0025] Segment 5 was identified as the coat protein gene based on N-terminal amino acid sequence and amino acid composition data (Chu *et al.*, 1993a). Segments 2 and 6 encode proteins containing the characteristic NTP-binding motifs and thus are predicted to be the putative viral replication-associated protein (RAP) genes. The remaining 4 DNA components are unrelated to each other or to segment 2, 5 and 6, based on their distinctive deduced amino acid sequence. The SCSV DNAs have no significant nucleotide sequence homology with the genomes of geminiviruses although some homology exists at the deduced amino acid level.

[0026] The replicative competency of SCSV has been demonstrated (Chu *et al.*, 1993b). Since the SCSV virion DNA is single-stranded and the transcripts are of viral sense, the first likely biosynthetic event after uncoating is likely to be the synthesis of the replicative form DNA using host DNA polymerase. (The DNAs of SCSV have the ability to self prime in dsDNA synthesis [Chu and Helms, 1988]). Host RNA polymerase is thought to bind to the promoters initiating RNA transcription followed by synthesis of the viral proteins required for virus multiplication.

[0027] In a particularly preferred embodiment of the present invention, there is contemplated an SCSV promoter or promoter-like sequence comprising a nucleotide sequence selected from within SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and SEQ ID NO: 7 and/or genetic constructs comprising same.

[0028] A "promoter-like sequence" as used herein includes any functional mutant, derivative, part, fragment, homologue or analogue of a naturally occurring SCSV promoter. Promoter-like sequences contemplated herein include single or multiple nucleotide substitutions, deletions and/or additions to an SCSV promoter, provided that the said promoter-like sequences retain at least 35%, preferably at least 45%, more preferably at least 55%, even more preferably at least 65-70% and still more preferably at least 85-95% or greater promoter activity compared with the corresponding wild-type SCSV promoter.

[0029] In yet another embodiment, there is provided a genetic construct comprising an SCSV promoter or promoter-like sequence and which is operable in a plant cell, said promoter or promoter-like sequence corresponding to all or part of any one of SEQ ID NO: 1 to 7 or capable of hybridising under a range of stringency conditions, ranging from high to low stringency conditions to at least one of SEQ ID NO: 1 to 7. Conveniently, a mutant, derivative, part, fragment, homologue or analogue of an SCSV promoter is defined as being functional in a plant cell and capable of hybridising under a range of at least high to low stringency conditions to at least one of SEQ ID NO: 1 to 7.

[0030] In a particularly preferred embodiment, the genetic construct further comprises a termination and/or polyadenylation sequence from SCSV or from non-SCSV source and which enhances or other facilitates expression of a gene operably linked to said promoter.

[0031] For the purposes of defining the level of stringency, reference can conveniently be made to Sambrook *et al* (1989) which is herein incorporated by reference where the washing steps at pages 9.52-9.57 are considered high stringency. A low stringency is defined herein as being in 0.1-0.5% w/v SDS at 37-45°C for 2-3 hours. Depending on the source and concentration of nucleic acid involved in the hybridisation, alternative conditions of stringency may be employed such as medium stringent conditions which are considered herein to be 0.25-0.5% w/v SDS at $\geq 45^{\circ}\text{C}$ for

2-3 hours or high stringent conditions as disclosed by Sambrook *et al* (1989).

[0032] Another embodiment of the present invention contemplates a method of expressing a foreign gene in a plant cell, said method comprising introducing into said plant cell a genetic construct comprising and SCSV promoter or promoter-like sequence operable in said plant cell and operably linked to said foreign gene. In a further embodiment, multiple SCSV promoters are used to drive one or more transgenes without antagonism. In yet a further embodiment, the SCSV promoter is associated with the SCSV segment 2 gene in order to enhance the expression of the foreign gene. In another embodiment, the genetic constructs further comprises one or more termination and/or polyadenylation sequences which are located at the 3' end of the foreign gene. These sequences enhance or otherwise facilitate expression of the foreign gene. The termination and/or polyadenylation segment may be from SCSV or from another source such as the *F. bidentis* MeA gene.

[0033] In still yet another embodiment, the present invention contemplates a transgenic plant carrying an SCSV promoter or promoter-like sequence as hereinbefore defined in its genome and optionally a termination and/or polyadenylation sequence to enhance expression of a gene downstream of said promoter. Preferably, the transgenic plant exhibits altered characteristics due to expression of a genetic sequence such as a gene, oligonucleotide or ribozyme downstream of the SCSV promoter.

[0034] The present invention is further described by reference to the following non-limiting figures and/or examples. Reference herein to a promoter region from SCSV is abbreviated to "S" for SCSV, the genome segment number (e.g. 1, 3, 4, 5 and 7) and "nc" for non-coding region. For example, the promoter from SCSV genome segment 1 is defined as "S1nc". Terminator sequences for particular SCSV genome segments are indicated for example, as follows: "SC1Tr" or "SC5Tr" for the terminator sequences for segments 1 and 5, respectively. Genetic constructs comprising an SCSV promoter, a reporter gene such as *GUS* and a terminator sequence such as from SCSV is abbreviated to "SCSV:*GUS*:SCTr" or "SCSV:*GUS*:SCSVTr". Specific promoters and termination sequences are defined as above, for example S4nc:*GUS*:SC1Tr or S4nc:*GUS*:Me3", "S4nc:*GUS*:Me3". In the latter construct the terminator sequence from the MeA gene of *Flaveria bidentis* is used, referred to herein as "Me3".

[0035] In the Figures:

FIGURE 1 shows the structures and transcription units found in a representative DNA component of a typical geminivirus and SCSV, both of which contain a ssDNA genome.

FIGURE 2 shows the seven DNA segments found in the genome of SCSV in a linear form, indicating the positions of the stem-loop structure, the common region, the open reading frame (ORF), the TATA box and the termination and polyadenylation signals on each DNA.

FIGURE 3 shows the construction of the seven SCSV DNA non-coding region: β -glucuronidase (*GUS*) fusion expression vectors for transformation into tobacco plants. The amplified PCR fragments were separately cloned in front of the *GUS* gene in pHW9 at the BamHI (B) and NcoI (N) sites as indicated. The resultant recombinant pHW9 vectors were cut at the EcoRI site and cloned into the EcoRI site of the recipient PGA470 binary vector.

FIGURE 4 shows the construction of the segments 5 and 7 promoter:*GUS* fusion expression vectors and their deletion derivatives for protoplast studies. DNAs corresponding to the full-length non-coding regions were obtained by PCR and cloned into pKGO in front of *GUS* by blunt end ligation at the SalI site as indicated. The deletion derivatives were obtained by digesting the pKGO clones containing the full-length sequence with HindIII or PstI on the vector and the appropriate restriction enzymes on the SCSV sequence as indicated. The deleted pKGO constructs were religated after end-filling as required.

FIGURE 5 shows the construction of the recombinant binary pTAB10 vector (pBS150) containing the seg 7 promoter(57nc):*GUS* fusion gene for transformation into subterranean clover plants. The 57nc:*GUS* expression cassette was excised from the pKGO construct (Fig. 4) by digestion with HindIII and BamHI and blunt-end ligated to pTAB10 at the EcoRI site after end-filling the DNAs.

FIGURE 6 shows the complete sequences of the seven SCSV DNA circles. The sequence of the non-coding region on each DNA used in the construction of the expression cassettes are underlined.

FIGURE 7 shows *GUS* expression detected by histochemical staining on leaves of transgenic tobacco and subterranean clover transformed with the SCSV seg 7 promoter(S7nc):*GUS* fusion expression cassette.

FIGURES 8A to 8F are photographic representations of histochemical staining for *GUS* activity in transgenic plants - bright field. Bright field exposures of stained leaf pieces (L), stem sections (S), roots (R) and pollen (P) from

tobacco plants transformed with the GUS fusion constructs containing the SCSV promoter regions from segments 1, 3, 4, 5 and 7 referred to as S1nc, S3nc, S4nc, S5nc and S7nc promoter regions and from non-transformed plants (NT). Blue colouration indicates GUS expression. Each leaf, stem or root piece represents an independent transformant (except the top two root pieces of S5nc which could not be separated easily) and the pollen samples were mixtures from two or more transformants. Fig. 8a shows differential expression of GUS in plants transformed with either S4nc or S5nc regions compared to a non-transformed plant (NT).

FIGURES 9A to 9E are photographic representations showing histochemical staining for GUS activity in transgenic plants - dark field. Transverse (T) and longitudinal(L) thin sections of stained, embedded stem pieces from tobacco plants transformed with the GUS fusion constructs containing the component 1 (S1nc), 3 (S3nc), 4 (S4nc), 5 (S5nc), and 7 (S7nc) promoter regions, viewed with a dark field. Pink crystals indicate GUS expression. The stem pieces used for the transverse and longitudinal sections represent independent transformants. The magnifications are: 375X in S1nc T and L, S3nc L, S4nc T, S5nc T and L, and S7nc L; 480X in S3nc T; 200X in S4nc L; and 300X in S7nc T.

FIGURE 10 is a graphical representation of a fluorometric assay for GUS expression. Fluorometric assay results from leaf extracts of tobacco plants transformed with the GUS fusion constructs containing the component 1 (S1nc), 3 (S3nc), 4, (S4nc), 5 (S5nc), and 7 (S7nc) promoter regions. Each column represents an independent transformant. GUS activities were measured with a Labsystems Fluoroskan at 5 or 10 minute intervals over 60 minutes (or 30 minutes for S4nc) using 4-methylumbelliferyl β -D-glucuronide (MUG) as the substrate. The rates of GUS activity are expressed as fluorometric units (F1.U.) per minute per mg of protein. 1000 F1.U is approximately equal to 825 pmoles of 4-methylumbelliferone (MU).

FIGURE 11 is a diagrammatic representation of the SCSV segment 2 promoter (S2nc) construct capable of directing GUS expression in tobacco protoplasts. A fragment of segment 2 DNA from *NcoI*-*XbaI* was fused to the promoterless GUS vector, pKGO. Pr, promoter, seg 2, segment 2 of SCSV.

FIGURES 12a and 12b are diagrammatic representations showing constructs of SCSV:*GUS*:SCSV Tr expression vectors. The termination/polyadenylation sequences for segment 3 of SCSV (SC3Tr) and segment 5 (SC5Tr) were amplified by PCR and cut with the respective restriction enzymes and then cloned into recombinant pKGO vector as indicated. The SC3Tr construct was cloned as an *EcoRI*-*XhoI* fragment into the pKGo vector containing S1nc: *GUS*:OCS3' to make S1nc:*GUS*:SC3Tr. The SSC5TR construct was made as an *EcoRV* fragment into Vector pKGO containing S4nc:*Gus*:OCS3' to make S4nc:*GUS*:S5Tr.

FIGURES 13A to 13D are photographic representations showing GUS expression in potato plant tissues directed by the SCSV segment 4 promoter (S4nc). A. stem; B. leaf; C. stolon; and D. tuber.

FIGURE 14 is a photographic representation of GUS expression in cotton leaf directed by the SCSV segment 7 promoter (S7nc).

FIGURE 15 is a representation of the MeA3's terminator sequence of the *Flaveria bidentis* MeA gene (Me3). The stop codon is shown in bold face type at the beginning of the sequence. This sequence was engineered in the Chimeric construct to include an *EcoRI* site: GAATTCGTTTAG.... The chimeric constructs thus contained a sequence beginning AATTCGTTTAG.

FIGURE 16 is a diagrammatic representation of GUS expression vectors (ME20 and ME29) containing the indicated *Flaveria bidentis* MeA gene regulatory elements.

FIGURE 17 is a diagrammatic representation of the construction of S4nc plasmid pBS237 containing the expression cassette S4nc:*GUS*:Me3'. Plasmid pBS218 was digested with *EcoRI* to remove OCS3' region and ligated with an *EcoRI*.

FIGURE 18 is a diagrammatic representation of the construction of plasmid pBS246 containing the S1nc:nptII:SC3Tr expression cassette. The *Sall*-*Sall* fragment is approximately 8.5-9 kbp; B_L is about 0.5 kbp; B_R is about 0.6 kbp. SC1nc:nptII:SC3Tr is about 1.7 kbp.

FIGURE 19a-c are diagrammatic representations of the construction of plasmid pKHAN4 from pKHAN2 and pKSB. bar1, pKHAN4: A *HindIII*-*EcoRI* segment containing S7nc (572 bp), nptII coding region (978 bp) and vicillin 3' end

(276bp) from pKHAN2 was inserted into binary plasmid pKSB.bar1 to yield pKHAN4; pKHAN2. The nptII coding region (978bp, *Bam*HI-*Sma*I fragment) from p35SKN was cloned into Asp718 site (blunted with klenow fragment) of pKHAN1 to create pKHAN 2. SCSV Pro = S7nc; pKSB. Bar 1: pTAB10.MCSori1B digested with *Eco*R1 as ligated together.

FIGURE 20 is a photographic representation of a selection of Kanamycin resistant tobacco plants on regeneration medium transformed with binary vectors containing either 35S promoter:NPTII:35S terminator sequence (35SPrm: NPTII:35STrm) or S1nc:NPTII:SC3Tr expression cassette. (In the Figures, the abbreviations are 35S Prm NPTII35STrm and SC1 Prm NPTII Sc3 Trm, respectively.

FIGURE 21 is a diagrammatic representation of a cloning vector utilising SCSV DNA transcription regulatory signals.

FIGURE 22 is a diagrammatic representation of SCSV segment 2 dimer construct pBS2. This construct was created by cloning a tandem repeat of the SCSV segment 2 DNA (containing a whole functional seg 2 transcription unit) into the polylinker site of pGEM7 which was then cloned into a reduced version of the pMCP3 binary vector (Khan *et al.*, 1994).

[0036] A summary of the transcription activities facilitated by the SCSV transcription regulatory elements is shown in Table 19.

EXAMPLE 1

SCSV DNA sequence determination

[0037] The F isolate of SCSV (Chu *et al.* 1993a) was used for sequence determination. Full-length clones of the SCSV genome components were created from the replicative form (RF) DNA as described by Chu *et al.* (1993a). Other clones were created from the RF by PCR with SCSV specific primers designed from known sequences.

[0038] The dideoxy chain termination method (Sanger *et al.*, 1977) was used to sequence either M13 ssDNA templates (Sambrook *et al.*, 1989) or dsDNA templates prepared by the CTAB method (Del Sal *et al.*, 1989) from clones described above. Sequence analysis was carried out using the University of Wisconsin Genetics Computer Group Sequence Analysis Software Package (Devereaux *et al.*, 1984).

EXAMPLE 2

Plasmid construction

[0039] DNA manipulation techniques used were as described by Sambrook *et al.* (1989). The entire non-coding regions of all 7 DNA segments of SCSV were amplified by PCR using specific primers (See Table 8) with appropriate restriction enzyme recognition sites for cloning into the plasmid vectors. The amplified DNA fragments were separately cloned into the respective expression vectors upstream of a promoterless GUS reporter gene in the appropriate orientation to produce the SCSV promoter-GUS fusion constructs as shown in the Figures 3 and 4. The expression vector pHW9 (Fig. 3) followed by cloning into the binary vector pGA470 (An *et al.*, 1985) were used for tobacco transformation. The expression vector pKGO was used for GUS expression in protoplasts (Fig. 4) and the binary vector pTAB10 was used for subterranean clover transformation (Fig. 5). pKGO was constructed by cloning the *Xho*I fragment of pKIWI101 (Janssen and Gardner, 1989) containing the GUS gene and the OCS terminator sequence into the *Sa*II site of pJKKm (Kirschman and Cramer, 1988). Corresponding plasmids containing the 35S promoter fused to GUS were used as controls. The junctions of the clones were checked by sequencing. A promoterless GUS construct was used as a control.

[0040] Deletion derivatives of the SCSV segments 5 and 7 promoters were made by digesting the full-length non-coding sequence with an appropriate enzyme to produce the desired deletion (Fig. 4).

[0041] To investigate the phenomenon of transactivation, the S5nc:*GUS* expression cassette was excised from recombinant pKGO constructs and cloned into a pGEM plasmid containing the seg 2 RAP coding region expressed from the 35S promoter. The resultant plasmid carrying both the SCSV promoter:*GUS* and the 35S promoter:seg 2 RAP expression cassettes were electroporated into protoplasts.

EXAMPLE 3**Protoplast isolation and transient gene expression**

5 [0042] Recombinant plasmids were extracted from *E. coli* by alkaline lysis followed by purification through Qiagen columns as described in the Qiagen Plasmid Handbook.

[0043] Suspension cell cultures were used to isolate *Nicotiana plumbaginifolia* (Last *et al.* 1991) and subterranean clover cv. Woogenellup protoplasts (Chu *et al.* 1993b). Purified plasmids were electroporated into protoplasts of subterranean clover or *Nicotiana plumbaginifolia* as described by Taylor and Larkin (1988). Protoplasts were harvested 3 days later and assayed fluorometrically for transient GUS activity using 4-methyl umbelliferyl β -glucuronide as substrate (see below). All experiments were done using duplicate samples per treatment.

EXAMPLE 4**Transformation of tobacco with SCSV-promoter-GUS fusion constructs**

15 [0044] The recombinant pGA470 binary constructs containing the various SCSV promoter:GUS expression cassettes were separately transformed into *Agrobacterium tumefaciens* strain LBA4404 (Hoekema *et al.* 1983) by electroporation as described by Nagel *et al.* (1990). *Nicotiana tobacum* cv. Wisconsin 38 were transformed and regenerated as described by Ellis *et al.* (1987).

EXAMPLE 5**Transformation of subterranean clover with SCSV-promoter-GUS fusion construct**

25 [0045] The recombinant pTAB10 binary vector containing the S7nc:GUS fusion construct (pBS150) was transformed into *Agrobacterium tumefaciens* strain AGL1 (Lazo *et al.* 1991) by triparental mating (Ditta *et al.* 1980). Subterranean clover cv. Larisa was transformed by *Agrobacterium*-mediated transformation and regenerated as described by Khan *et al.* (1994).

EXAMPLE 6**GUS assays**

35 [0046] Protoplasts were lysed by sonication in the presence of 0.3% v/v Triton X-100 immediately after harvest. GUS activity of the soluble extract was determined in a fluorometric assay using the substrate 4-methyl umbelliferyl β -D-glucuronide (MUG) (Jefferson *et al.*, 1987). Fluorescence was measured using a Labsystem Fluoroskan II spectrophotometer.

[0047] GUS expression in intact transgenic tissues was detected by histochemical staining in 5-bromo-4-chloro-3-indolyl- β -glucuronic acid (X-gluc) (Jefferson *et al.*, 1987) and by fluorometric assay of the soluble extract using MUG.

EXAMPLE 7**Sequence of SCSV non-coding region**

45 [0048] The complete sequences of all the 7 known SCSV DNA circles have been determined (Fig. 6). Each DNA contains a non-coding region with signals (TATA boxes) for promoter activity (Table 2). These sequences have not been described or isolated before. Sequence comparison of the non-coding regions comprising these promoters showed that segments 3 and 5 are most similar, sharing 258 conserved nucleotides out of an average of 491 nucleotides in the non-coding regions of the DNAs. Segments 3, 4, 5 and 7 contain 170 conserved bases between them while only 152 bases are conserved between Segments 1, 3, 4, 5 and 7. The sequence variations in the non-coding regions of the SCSV DNAs suggest that the transcription and replication of the different SCSV genes may be regulated differently.

EXAMPLE 8**Transient activity of SCSV promoters in protoplasts**

55 [0049] The promoter activities of two SCSV DNA non-coding regions have been demonstrated directly by transient

expression of GUS using SCSV promoter: *GUS* fusion constructs in subterranean clover (Table 3) and tobacco protoplasts (Table 4). These results showed that both segment 5 and segment 7 promoters are functional in the absence of other SCSV DNA components. The SCSV promoters are also functional in protoplasts of either a natural host (subterranean clover) or a non host (tobacco). In tobacco protoplasts, the segment 7 promoter was similar in activity to the 35S promoter while the segment 5 (coat protein) promoter consistently showed activity about half that of the CaMV 35S promoter (Table 4). However, the activity of both promoters were higher in subterranean clover protoplasts, with the activity of the segment 7 promoter showing up to several times that of the 35S promoter (Table 3), suggesting that SCSV promoters work better in certain legumes than the widely used 35S promoter. The activity of the segment 7 promoter also appeared to be more variable in subterranean clover protoplasts than the others tested.

[0050] Plasmids containing various deletion derivatives of the non-coding sequence of segments 5 and 7 fused to *GUS* were also constructed (Fig. 4) and electroporated into protoplasts (Table 5). *GUS* assays of protoplasts transfected with these constructs showed that neither the stem-loop nor the common region were necessary for promoter activity although the latter was required for full activity (Table 5). The DNA sequence required for high level promoter activity appears to be less than 300 bp which is smaller than that required for other promoters, such as 35S promoter (Odell *et al.*, 1985).

EXAMPLE 9

Transactivation of SCSV promoter activity by SCSV segment 2 gene product

[0051] When co-electroporated with a 35S promoter:seg 2 RAP gene construct, the activities of *GUS* driven by the seg 5 promoter apparently increased by about 2 fold in both subterranean clover and tobacco protoplasts (Table 6). The segment 7 promoter activity may also be increased when co-electroporated with the 35S:seg 2 RAP construct but further experiments are needed to confirm this.

[0052] Transactivation of *GUS* activity was also apparently observed when the S5nc:*GUS* construct was co-electroporated with a binary vector plasmid (pBS2) containing a tandem repeat (dimer) of the segment 2 DNA (Table 6). A map of SCSV segment 2 dimer construct -pBS2 is shown in Figure 22. This construct was created by cloning a tandem repeat of the SCSV segment 2 DNA (containing a whole functional seg 2 transcription unit) into the polylinker site of pGEM7 which was then cloned into a reduced version of the pMCP3 binary vector (Khan *et al.*, 1994). The results suggest that both SCSV promoters are expressed concurrently. Thus, different SCSV promoters can either be used in combination with a 35S promoter or be used simultaneously to facilitate concurrent expression of multiple transgenes in plants. In contrast, reduced transgene activity has been observed when the 35S promoter is used in multiple or multiple copy transgenes (Linn *et al.*, 1990; Matzke and Matzke, 1991; Scheid *et al.*, 1991; Carvalho *et al.*, 1992).

EXAMPLE 10

Activity of SCSV promoters in transgenic plants

[0053] All the SCSV promoters, except those from segments 2 and 6, have been shown to be capable of driving expression of transgenes in tobacco plants (Fig. 7). The level of activity of the promoters measured by the MUG assay varied from plant to plant and from one promoter to another but is generally lower than that of the 35S promoter (Table 7).

[0054] Histochemical staining of intact transgenic tobacco tissues showed that the activity of the S4nc promoter appears to be constitutive and *GUS* activity was detected in all plant organs. The others are generally restricted to the vascular tissues although expression is also detected in pollen.

[0055] In transgenic subterranean clover plants expressing the S7nc:*GUS* gene construct, histochemical staining showed that *GUS* activity is found in leaves, stems and petioles. The distribution of *GUS* activity is mostly constitutive although in some tissues, the activity is largely in vascular tissues (Figure 7). In these plants, the level of promoter activity also varies from plant to plant but the activity is generally comparable to that of the 35S promoter.

[0056] These results indicate that the SCSV promoters provide a choice of promoters that can be used either independently or simultaneously to control the expression of one or more foreign genes in a wide range of plants and tissue types. Legumes are a major target for application. The activity of these promoters also can be enhanced by the presence of the seg 2 gene product. Thus, these promoters appear to have significant advantages over the CaMV 35S promoter, both in levels of expression, size and in overcoming some negative features of the 35S promoter. They would be applicable in a wide range of transgenic applications.

TABLE 1

Properties of plant viruses with small and multiple encapsidated circular ssDNAs (Plant Circoviruses)					
Virus	Hosts	Vector	No. of circles	Size (kb)	Coat protein (kDa)
FBNYV	Legumes	Aphids	2+	1	22
MDV	Legumes	Aphids	1+	1	21
SCSV	Legumes	Aphids	7	1	19
BBTV	Monocots	Aphids	6+	1-1.2	20
CFDV	Monocots	Planthopper	1+	1.3	25

[0057] Compiled from data presented at the Sixth International Congress of Plant Pathology, Montreal, July, 1993. FBNYV = faba bean necrotic yellow virus, MDV = milk vetch dwarf virus, SCSV = subterranean clover stunt virus, BBTV = banana bunchy top virus, CFDV = coconut foliar decay virus.

TABLE 2
Transcription units and putative gene functions of the SCSV DNA segments

DNA Segment	Segment (bases)	Function	Non-Coding Region		TATA Box		ORF		Termination Codon	Polyadenylation Signal
			(bases)	Pos ^a	Sequence	Pos ^b	# aa	Mr (kDa)		
1	1001	Unknown	661	201	TATAAAT	48	112	12.7	TGA	AATTAT
2	1022	Replication	178	-8	TATATAT	102	280	32.5	TGA	AATAAA
3	991	Unknown	495	326	TATAAAT	57	164	19.1	TGA	AATAAA
4	1002	Unknown	539	285	TATAAAT	71	153	17.7	TAA	AATAAA
5	998	Coat protein	487	330	TATAAAT	48	169	18.7	TAA	AATAAA
6	1017	Replication	158	-7	AATATAA	66	285	33.5	TGA	AATAAA
7	988	Unknown	546	324	TATAAAT	67	146	16.9	TAA	AATAAA

^a Position of the TATA box is the number of bases from the first nucleotide of the stem-loop to and including the first base of the TATA box. See Fig. 1 for a graphic presentation of the genome segments.

^b Position of the ORF is the number of bases from the first base of the TATA box to and including the first base of the initiation codon.

TABLE 3

SCSV promoter directed GUS activity in subterranean clover protoplasts					
	GUS Activities				
Treatments	Expt 1		Expt 2		Average
	Act	%35S	Act	%35S	%35S
No DNA	10	0%	13.1	0%	0%
35S: <i>GUS</i>	27.3	100%	36.6	100%	100%
S5nc: <i>GUS</i>	22.6	73%	40.2	116%	95%
S7nc: <i>GUS</i>	36	147%	117	385%	266%

[0058] All experiments were done using duplicate samples per treatment. GUS activity was measured using a Lab-system Fluoroskan II spectrophotometer and is presented both in absolute activity (Act) and as a percentage of 35S:*GUS* activity (%35S). constructs are represented as "promoter:reporter gene". For example, "35S:*GUS*" is the 35S promoter and the GUS reporter gene. "S5nc" and "S7nc" are the promoters for segments 5 and 7, respectively of SCSV.

TABLE 4

SCSV promoter directed GUS activity in tobacco protoplasts					
	GUS Activities				
Treatments	Expt 1		Expt 2		Average
	Act	%35S	Act	%35S	%35S
No DNA	13.8	0%	10.5	0%	0%
35S: <i>GUS</i>	113	100%	117	100%	100%
S5nc: <i>GUS</i>	52.3	39%	61	48%	44%
S7nc: <i>GUS</i>	93	80%	106	90%	85%

[0059] All experiments were done using duplicate samples per treatment. GUS activity was measured using a Lab-system Fluoroskan II spectrophotometer and is presented both in absolute activity (Act) and as a percentage of 35S:*GUS* activity (%35S).

TABLE 5

Promoter activities (GUS expression levels) of deletion derivatives of segment 5 and 7 non-coding regions in protoplasts. Levels are expressed as percentages of the activity of the respective full-length non-coding sequence.					
		GUS Activity			
		Tobacco		Subclover	
Promoter	Deletion ^a	Expt 1	Expt 2	Expt 1	Expt 2
Segment 5	dNde	101	110	-	-
	dPml (stem-loop)	65	88	-	-
	dAfl (Stem-loop+ common region)	70	102	63	91
	dPst	5	18	6	4
Segment 7	dAfl (stem-loop+ common region)	50	55	67	39

^a See Figure 4 for maps of deletion derivatives.

TABLE 6

Transactivation of segment 5 promoter activity (GUS expression) in tobacco and subterranean clover protoplasts by gene product of segment 2.					
		GUS Activity ^a			
Promoter Construct	Protoplasts	Expt 1	Expt 2	Expt 3	Expt 4
S5nc: <i>GUS</i>	Tobacco	100	100	-	-
S5nc: <i>GUS</i> + 35S:Seg 2 RAP	Tobacco	262	217	-	-
S5nc: <i>GUS</i>	Subclover	100	100	100	100
S5nc: <i>GUS</i> + 35S:Seg 2 RAP	Subclover	132	176	188	770
S5nc: <i>GUS</i> + Seg 2 dimer ^b	Subclover	-	-	-	320

^a GUS activities are expressed as percentages of the S5nc:*GUS* construct in each experiment

^b See Example 9

TABLE 7

Relative GUS activity in leaf extracts of independent transgenic tobacco plants containing different promoter: <i>GUS</i> constructs as determined by fluorometric assays ^a			
Promoter		GUS Activity	Average
Non transgenic control		123	
35S	Average		123
	#3	38,431	
	#6	20,052	
	#8	20,648	
	#11	28,325	
	#12	24,700	
S4nc	Average		26,431
	#1	7,229	
	#2	4,690	
	#5B	4,300	
	#9	6,218	
	#18	4,895	
	#19	6,098	
S7nc	Average		5,572
	#4	642	
	Average		642

^a GUS activity presented is the best 25% of the transgenic plants tested.

EXAMPLE 11

Further characterisation of SCSV promoter activities in transgenic plants

[0060] Transgenic plants of tobacco transformed with the five (Segments 1, 3, 4, 5 and 7) SCSV promoter:*GUS* fusion cassettes were assayed for GUS activity by both histochemical (Figs. 8 and 9) and fluorometric assays (Fig. 10). Samples taken from tissue-cultured and young glasshouse-grown plants produced the same GUS expression pattern. GUS activity was observed in all plant parts, including roots, stems, leaves, petioles and all flower parts. Promoter 5 construct gave relative lower GUS expression in pollen than other promoters. The results from fluorometric assays confirmed previous data showing that segment 4 promoter was the highest expressor, with activity 10-fold or

greater than the rest (Fig. 10), but is still lower than that of the 35S promoter. The expression levels of the segment 1, 3, 5 and 7 promoters were comparable to those of the phloem-specific promoter *rolC* in tobacco (Schmulling *et al.*, 1989; Sugaya *et al.*, 1989). Plants transformed with the promoterless GUS construct did not express GUS by either assay method. Histochemical assays showed that expression of all promoter constructs was the highest in vascular tissues, with high expressors being more constitutive than low expressors which are more vascular-limited (Fig. 8). In general, promoter 1, 3, 5 and 7 constructs are expressed mostly in the vascular tissues. In particular, GUS expression by promoter 1 and 3 constructs are mainly restricted to phloem tissues. However, for all promoters histochemical staining of leaves showed that GUS expression in these tissues are often blotchy (constitutive and vascular-limited) and variable between leaves of the same plant. Dark field microscopy (Jacobsen-Lyon *et al.*, 1995) also showed that none are strictly vascular-limited (Fig. 9).

[0061] Twenty primary transgenic subterranean clover plants expressing the seg 7 promoter:*GUS* gene were further characterised by histochemical assays (Table 9). These assays showed that GUS activity was observed in all plant parts, including roots, stems, leaves and petioles. GUS expression was the highest in vascular tissues, with some leaves being more constitutive and blotchy than other organs and high GUS expressing plants being more constitutive than low expressing ones. Samples taken from tissue-cultured and glasshouse-grown plants produced the same GUS expression pattern.

EXAMPLE 12

Detection of promoter activity in SCSV segment 2 DNA

[0062] Experiments showed that the non-coding regions from the SCSV segments 2 and 6 DNAs were unable to drive the expression of GUS gene in transgenic tobacco. These regions are only 179 and 159 nucleotides long, respectively, and it is likely that additional sequences are required for promoter activity. To test this hypothesis, a new segment 2 promoter sequence was constructed consisting of the DNA fragment from nucleotides 526 to 46 and fused to the promoterless GUS vector pKGO (Fig. 11). The fusion construct was electroporated into tobacco protoplasts. Gus activity was detected in electroporated tobacco protoplasts at levels similar to that of segment 5 promoter:*GUS* construct (Table 10).

[0063] A binary vector containing the above SRnc promoter:*GUS* fusion DNA was also transformed into tobacco plants as described in Example 4. Histochemical staining of several transformed tobacco plants showed that GUS expression was mainly vascular. These results showed that additional sequence from the SCSV segment 2 DNA coding region is necessary for promoter function. Since the SCSV segment 6 is a variant of the segment 2, it is expected that a similar construct comprising the noncoding and part of the coding region of this DNA will produce an active promoter. Thus, all SCSV promoters are expected to be suitable for driving gene expression in plants.

EXAMPLE 13

Enhancement of gene expression by SCSV transcription termination and polyadenylation signals

[0064] Effective gene expression requires not only a promoter, but also specific nucleotide sequences at the 3' end of the coding region of the gene, known as the termination and polyadenylation signals (Messing *et al.*, 1983; Joshi 1987b; Gil and Proudfoot, 1984; Rothnie *et al.*, 1994). These special sequences are required to signal the RNA polymerase to stop transcription and to allow further processing of the RNA transcript. The activity of the termination and polyadenylation signals may affect the transcription efficiency and stability of the RNA being transcribed. Some widely used termination/polyadenylation sequences include those from the NOS (Depicker *et al.*, 1982), OCS (Janssen and Gardner, 1989) and CaMV 35S (Pietrak *et al.*, 1986) genes.

[0065] Each of the SCSV DNA segment (or component) contained a terminator sequence comprising a termination and a polyadenylation signal sequence in the noncoding region (Table 11; Figure 2). To demonstrate activity of the termination/polyadenylation signals in SCSV DNA, GUS expression vectors containing either the segment 3 or segment 5 polyadenylation and termination signal (Fig. 12) was constructed and subjected to transient expression in tobacco protoplasts. The respective terminator sequence was amplified by PCR with several restriction sites incorporated into the primers (Fig. 12). The amplified terminator fragments were cut with the indicated restriction enzymes and cloned into the pKGO recombinant plasmid containing either S1nc or S4nc promoter:*GUS*:OCS3' constructs, from which the OCS3' sequence has been deleted (Fig. 12). The resultant S1nc:*GUS*:SC3Tr (the segment 1 promoter here carries a deletion of the *HindIII* fragment from nucleotides 641-782 which has no effect on GUS activity) and S4nc:*GUS*:S5Tr constructs were electroporated into tobacco protoplasts and assayed for GUS activity. The results showed that GUS activity was increased 2 to 3-fold when the SCSV termination/polyadenylation sequence was used instead of the commonly used OCS termination/polyadenylation sequence in the same construct (Table 12). In the same experiment, the

construct S1nc:*GUS*:S3Tr produced over two-fold higher activity than the 35S:*GUS*:OCS3' construct (Table 12). These results indicate that each of the SCSV DNA components contains a different termination and polyadenylation signal sequence which can be used in various combination with the SCSV promoters to regulate and/or enhance expression of foreign genes in plants. As with the SCSV promoter sequences, the SCSV termination/polyadenylation sequences are advantageous over currently available termination/polyadenylation sequences by their small sizes (160-170 nucleotides) and the availability of a broad range of transcription regulators with different strengths and tissue specificities for genetic manipulation. The results also show that the use of a SCSV promoter in combination with a SCSV terminator sequence in higher levels of gene expression than constructs using the 35S promoter in conjunction with one of the common transcription terminator sequences.

EXAMPLE 14

Activity of SCSV promoters in transgenic potato plants

[0066] pGA470 binary vector containing the S4nc:*GUS*:NOS fusion construct cloned in pHW9 (Figure 3) was used to transform potato plants. pHW9 is derived from pHW8 (Dolferus *et al.*, 1994) into which the polylinker from pGEM3zf (+) is inserted. The recombinant binary vector was transformed into *Agrobacterium tumefaciens* strain LBA4404 by electroporation (Nagel *et al.*, 1990). Potato cultivars Atlantic and Sebago were transformed and regenerated essentially as described by Wenzler *et al.* (1989) except for the following modifications. Stem pieces instead of leaf pieces were used for transformation and 10 mg/l of benzylaminopurine (BAP) instead of 2.24 mg/l was used during co-cultivation. After co-cultivation, stage 1 medium is supplemented with 100mg/l of cefotaxime and not kanamycin or carbenicillin. Stage II medium contained 2 mg/l BAP, 5 mg/l GA3, 100 mg/l kanamycin and 100 mg/l cefotaxime.

[0067] Six transformed plants comprising 5 of cultivar Atlantic and 1 of cultivar Sebago were transferred and grown in the glasshouse for 10-11 weeks until small tubers formed. Tissues from different parts of the plants were assayed by histochemical GUS staining. The results showed that GUS was highly expressed in all plant parts including roots, stolons, tubers, stems and leaves but the expression was predominantly vascular, including cambium, phloem elements and some xylem elements (Fig. 13). As in other transgenic hosts, GUS expression in non-vascular tissues of highly GUS active plant materials, especially young tubers, was more evident than in less active tissues when compared with plants transformed with a 35S:*GUS*:NOS construct, SCSV promoter directed *GUS* expression in tubers was at least as high as that of the 35S:*GUS* construct.

EXAMPLE 15

Activity of SCSV segment 7 promoter in transgenic cotton plants

[0068] pGA470 binary vector containing S7nc:*GUS*:NOS fusion construct cloned in pHW9 was used to transform cotton plants. The recombinant binary vector was transformed into *Agrobacterium tumefaciens* strain AGL 1 by triparental mating. Cotton (*Gossypium hirsutum*) cv. coker 315 was transformed and regenerated as described by Cousins *et al.* (1991).

[0069] Transformed plants were grown in the glasshouse and leaf tissues from 18 independent transgenic plants were assayed for GUS activity by histochemical staining. GUS activity varied between plants. Five of these plants showed strong GUS expression, similar in range to 35S promoter driven GUS expression and was predominantly in the vascular tissues (Fig. 14). GUS activity was especially strong in the gossypol glands. As in other transgenic hosts, GUS staining in highly expressed tissues were also constitutive.

[0070] A variety of tissues from these plants were then stained and vascular expression was observed in all organs including roots, stems, petioles, petals and other vascularised floral parts. Expression appears to be particularly high in young flower buds. Seedlings from one of the lines was screened for GUS activity. All 10 progenies stained heavily in roots and leaves indicating that the gene was inherited and that the line probably contained more than one independent insertion site.

EXAMPLE 16

Stability of transformed SCSV promoter:*GUS* expression cassette in transgenic plants

[0071] The stability of GUS expression driven by the various SCSV promoters in transgenic tobacco and subclover were further characterised in T1 generation seedlings of subterranean clover and tobacco plants.

[0072] In tobacco, T1 seedlings from 10 independent transgenic lines were assayed by histochemical staining. The results showed that the expression of the GUS gene driven by all the five (segments 1,3,4,5 and 7) promoters was

stable in the T1 seedlings, with the pattern of expression being maintained in all cases between T0 and T1 plant tissues of the same age. In very young stems where the vascular tissues are not well differentiated, expression from all promoters were very high and was detected through out the stem tissues. Gradual vascular limitation occurs with age and with increasing differentiation of the vascular bundles. As with T0 plants, the segment 4 promoter mediated GUS

expression was more constitutive than others.

[0073] Fifty 2-3 month old T1 seedlings from 15 independent transgenic subclover plants expressing the S7nc:*GUS* fusion construct were assayed for GUS activity by histochemical and fluorometric assays. The results showed that the expression of the GUS gene driven by the segment 7 promoter was stable in T1 seedlings, with the pattern of expression being maintained between T0 and T1 plant tissues of the same age. GUS expression was found to generally segregate at the expected ratio of 3:1. The preliminary results from fluorometric assays confirmed the histochemical data suggesting that this segment 7 promoter construct had GUS activity somewhat lower than that of the 35S promoter in leaves and petioles (Table 13). GUS activity in subterranean clover stems, however, was 3-fold higher than in petioles and 6-fold higher than in leaves (Table 14). The age of the plants at the time of assay was 2 to 3 months.

EXAMPLE 17

Transient activity of SCSV promoter in soybean leaves

[0074] The SCSV promoter:*GUS* construct used (Table 15) was derived from the promoterless GUS plasmid pKGO (Figure 4; pJKKm(-) K1W1 GUS:OCS) described previously while the 35S promoter:*GUS* construct was pGUS. pGUS is derived by cloning the *Gus* gene from pKIWI101 into the plant expression vector pDH51 (Pietrzak *et al.*, 1986).

[0075] For transient GUS expression in soybean tissues, the GUS constructs were introduced into tissues by particle bombardment using the Bio-Rad Biolistic PDS-1000/He Particle Delivery System as above. A 50µl suspension containing 3mg of a 1:1 ratio of 1 and 5µ gold particles plus 6µg of DNA was shot onto plates containing 3 leaves each. Fully expanded leaves used in these experiments were prepared from 24 day old soybean plants cv. Wayne. After particle bombardment, GUS activity was assayed 24 hours later by vacuum infiltration of the leaves with X-Gluc (Craig, 1992).

[0076] The results (Table 15) showed that in transient expression in soybean leaves, SCSV segment 4 promoter was more active (25-35 spots/leaf) than the 35S promoter (10-15 spots/leaf) when the respective plasmids were shot into soybean leaves.

EXAMPLE 18

Testing of SCSV promoters for callus-specific expression

[0077] All seven SCSV non-coding sequences were cloned into the promoterless GUS vector pHW9. Binary vectors each containing one of the seven SCSV promoter:*GUS* fusion constructs were transformed into tobacco tissues by *Agrobacterium*-mediated gene transfer. At 2-3 weeks after transformation, calli containing primordia of transformed shoots were subjected to histochemical GUS staining. Best expression was observed in calli transformed with segment 1 followed by the S4nc:*GUS*:OCS constructs. This result suggests that the segment 1 promoter is best suitable for selectable marker gene expression and that the segment 4 promoter is best for gene expression.

EXAMPLE 19

Characterisation of regulatory sequences of the *Flaveria bidentis* MeA gene

[0078] In *Flaveria bidentis* (Chitty *et al.*, 1994) the MeA gene is the gene that codes for the NADP-malic enzyme adapted for C4 photosynthesis. The structure and putative promoter and transcription termination/polyadenylation signal sequences of this gene has been isolated and the terminator sequence determined (Fig. 15). The potential activities of the putative promoter element (MeA 5' sequences [MeA 5'] and the terminator MeA 3' sequences [MeA 3']) of the *F. bidentis* MeA gene were studied in transgenic *F. bidentis* plants using GUS expression vectors (Fig. 16). A long version of the MeA 3' terminator sequence (MeA 3'L = 5.5kb from the stop codon) was used in these experiments. In Fig. 16, the GUS expression cassette ME20 is ligated to the binary vector pGA470 (An *et al.*, 1985) while ME29 is cloned into pGA482 (An, 1986). Plants were transformed with these vectors as described by Chitty *et al.* (1994)

[0079] Study of GUS activity of the transformed plants by histochemical staining and fluorometric assays showed that the MeA 3' sequence of the gene is required for high level expression of GUS in leaves of transgenic *F. bidentis* plants (Table 16). The 5' sequences of the gene do not appear to contribute to gene expression in leaves but appear to direct expression in meristems and stems in the presence of a suitable transcription termination/polyadenylation

signal sequence such as the OCS 3' (Table 16).

EXAMPLE 20

Use of the MeA 3' termination/polyadenylation signal sequences in SCSV promoter constructs to enhance gene expression in monocotyledonous plants

[0080] Because most gene control elements are located at the 5' end, the activity of the MeA 3' sequence is tested in conjunction with the S4nc SCSV promoter with the view to enhance gene expression directed by the SCSV promoters. For these experiments, a short version of the MeA 3' terminator sequence was used (MeA 3'S; 900 bases from the stop codon) to prepare GUS expression vectors containing the S4nc promoter with either the OCS 3', SCSV segment 5 3' (SC5Tr) or the MeA 3' transcription termination/polyadenylation signal sequence. These constructs were derived from the promoterless GUS plasmid pKGO described previously and the recombinant plasmid pBS237 containing the S4nc:*GUS*:MeA3' construct is presented in Fig. 17. GUS activity conferred by these constructs were assayed in Japonica rice callus cv. Taipei 309. The constructs were introduced into rice calli by particle bombardment using the Bio-Rad Biolistic PDS-1000/He Particle Delivery System (Bio-Rad Laboratories) and compared with results obtained in dicotyledonous tissues such as soybean leaves and tobacco protoplasts (Table 17). For rice particle bombardment experiments, 4 mg of a 1:1 ratio of 1 and 5 micron gold particles plus 5 µg of DNA in a total of 50 µl volume was shot onto six plates of calli. The DNA was made up with a 4:1 molar ratio of each of the vectors containing GUS gene to the vector containing the selectable marker gene. The vector containing the selectable marker was pTRA151 (Zheng *et al.*, 1991). Each plate contained 50-100 fresh secondary calli derived from mature embryos. Forty hours after DNA bombardment, GUS activity was detected by placing the calli in 0.3% w/v X-Gluc solution in 100 mM phosphate buffer. Blue spots were counted after overnight incubation.

[0081] For transient GUS expression in tobacco and soybean, only the GUS constructs were introduced into protoplasts and leaf tissues, respectively. After electroporation, tobacco protoplasts were assayed for GUS activity as previously described. The constructs were introduced into soybean tissues by particle bombardment as described above.

[0082] The results showed that in the monocotyledonous rice tissues, a 16-fold higher activity was obtained with the MeA 3' construct compared to the SCSV terminator (Table 17). In similar experiments, a highly expressed GUS construct containing the ubiquitin promoter:*GUS*:NOS cassette (Christensen *et al.*, 1992) has about 4-fold higher activity than the SC4:*GUS*:MeA3' construct.

[0083] In the dicotyledonous tissues, similar activities were obtained with both of these constructs in tobacco protoplasts and soybean leaves. However, both were 2-fold higher in activity than that obtained with the OCS terminator in tobacco protoplasts (Table 17).

[0084] These results suggest that the MeA3' sequence can be used to enable gene expression directed by SCSV promoters in monocots.

EXAMPLE 21

Use of new vectors containing SCSV promoters and terminators to drive a selectable marker gene in transgenic plants

[0085] The suitability of using SCSV promoters to drive a selectable marker gene as a basis for selecting transgenic plants after transformation and regeneration was tested in tobacco plants. The selectable marker used is the kanamycin resistance gene, *nptII*. Binary vectors containing either a SCSV segment 1 (pBS246) (Fig. 18) or a SCSV seg 7 promoter (pKHAN4) (Fig. 19) fused to the *nptII* gene were constructed from the pART27 (Gleave, 1992) and pKSB.bar1 (Figure 19), respectively. These were transformed separately into tobacco plants (Ellis *et al.*, 1987) and putative transgenic plants were selected under kanamycin selection using 100 µg/ml kanamycin (Fig. 20). Kanamycin resistance was confirmed in the transgenic plants by dot blot assay for the *nptII* gene activity (McDonnell *et al.*, 1987) and survival of the transgenic plants under 100 µg/ml kanamycin in a rooting medium. The results showed that the SCSV segment promoter construct produced at least as many kanamycin resistant plants as the 35S promoter construct used in the same experiment and is, therefore, as effective as the 35S promoter for selecting transgenic tobacco plants based on kanamycin resistance (Table 18). Tobacco transformed with pKHAN4 is resistant to 100 µg/ml kanamycin in regeneration medium and 50 µg/ml kanamycin in rooting medium. Restriction maps of pKSB.bar1 and pKHAN2 used to produce pKHAN4 are shown in Figure 19.

EXAMPLE 22**Development of a new plant gene expression vector system**

5 **[0086]** A new expression vector comprising a SCSV segment 4 promoter and a SCSV segment 5 terminator driving any useful gene of interest (pICAN 1) (Fig. 21) has been constructed from a pGEM derivative and the resultant expression cassette can be inserted into the binary vectors pBS246 and pKHAN4. The resultant binary vectors can then be used to transform plants of economic importance especially cotton, subclover, potato and white clover under kan-
10 amycin selection. Other binary vectors can be constructed from different combinations of SCSV promoters and terminators to produce a full range of binary vector system for plant gene expression.

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TABLE 8

Sequences and positions of PCR primers for cloning non-coding regions and corresponding PCR fragment sizes.

Primer name	Position of 5' end	Primer 1 sequence (5'-3')	Primer 2 name	Position of 5' end	Primer 2 sequence (5'-3')	Fragment size (bp)*
S1nc3	241	GGCGTGCCTCGGCCATGG CGCTATGAAATTCTGAAC	S1nc5	577	GGCGTGCCTCGGCCATCCTA TGTTGTAATTTTATATGG	665
S2nc3	79	GGCGTGCCTCGGCCATGG AAGCTTAGAGAGAGAAAG	S2nc5	924	GGCGTGCCTCGGCCATCCA ATAAAGAATATATATTG	177
S3nc3	374	CTCACTATAGAACCATGGA CACAGATTCTAAG	S3nc5	863	CTCACTAAAGGGGATCCTG AGATGTAATTGTG	502
S4nc3	347	CTCACTATAGAACCATGGA AACGCAGAACAAAG	S4nc5	803	CTCACTAAAGGGGATCCTA ATTGTTATTATCA	546
S5nc3	372	CTCACTATAGAACCATGGT CGTTGTAAATGAC	S5nc5	874	CTCACTAAAGGGGATCCTA ATTGIGATGATT	523
S6nc3	50	CTCACTATAGAACCATGGT GGCCCAGGGAAGCGA	S6nc5	903	CTCACTAAAGGGGATCCTG AAACTCTGCGAA	164
S7nc3	383	CTCACTATAGAACCATGGC TTAAACCAGAACAA	S7nc5	817	CTCACTAAAGGGGATCCTA ATTAATAGTAATTATG	554

* not including the spacer nucleotides at the 5' ends of the primers

TABLE 9

GUS activity of SCSV segment 7 promoter: <i>GUS</i> construct in primary transgenic subterranean clover plants (To)		
Plant #	Basta Resistance	GUS Activity
1	R	+++
2	R	++
3	R	-
4	R	++
5	S	++
6	R	-
7	R	++++
8	R	++++
9	MR	+++
10	R	+++
11	R	+++
12	MR	-
13	MR	++
14	S	++
15	R	+
16	N.d.	++++
17	N.d.	+++
18	N.d.	-
19	N.d.	+++
20	N.d.	++
Plants were analysed two months after transfer of plants to glasshouse from tissue culture. Basta (phosphinothricin - [PPT] resistance was assayed by painting basta at 1 gm PPT/litre onto fully unfolded young leaves and reaction was assayed after one week. R No damage; MR Moderate damage to leaflet; S Leaflet dead N.d. Not determined		

TABLE 10

GUS activity in tobacco protoplasts directed by SCSV segment 2 promoter to tobacco protoplasts relative to the 35S promoter		
Construct	GUS Activity	
	Experiment	
	1	2
S2nc: <i>GUS</i> :OCS3'	0.46	0.45
35S: <i>GUS</i> :OCS3'	1	1

TABLE 11

Putative Polyadenylation and Termination signals in SCSV DNA Components

DNA Component	Putative Polyadenylation/Termination Signals
Seg. 1	AATTAT <u>19</u> TGTGTTTT
Seg. 2	AATAAA <u>10</u> TTGTTTT
Seg. 3	AATAAA <u>3</u> TTGTT
Seg. 4	AATAAA <u>8</u> TTATTGTT
Seg. 5	AATAAA <u>3</u> TTGTTTT
Seg. 6	AATAAA <u>9</u> TTGTT
Seg. 7	AATAAA <u>11</u> TTGTTT

TABLE 12

GUS Activity Directed by SCSV Promoter in the presence of different terminators
in tobacco protoplasts

GUS ACTIVITY				
	Expt 1	Expt 2	Expt 3	Av
S4nc:GUS:OCS3'	551	166.3	-	358
S4nc:GUS:SC5Tr	1258	311.8	-	785
No DNA	0	0	0	0
S1nc:GUS:OCS3'	-	-	26	26
S1nc[ΔHindIII] ^a :GUS:OCS3'	-	-	29	29
S1nc[ΔHindIII]:GUS:SC3Tr	-	-	84	84
35S:GUS:OCS3'	-	-	35	35

In each experiment, duplicate electroporations of each construct was performed.
Results are the average of the duplicates.

^a Contains a deletion of a HindIII fragment.

TABLE 13

Fluorometric GUS Assay of Independent T1 generation of transgenic subterranean clover plants expressing either the S7nc:GUS or the 35S:GUS Construct

Construct/Plant #	Leaf (Young) [unfolded]	Petiole (Young) [unfolded]
S7nc:GUS Plant # 1	56.6	120
S7nc:GUS Plant # 2	35	48
S7nc:GUS Plant # 3	116	140
35S:GUS Plant # 1	120	238
35S:GUS Plant # 2	280	238

Plants were 2 - 3 months old when assayed.

Results show differential expression in different tissues.

TABLE 14

Distribution of GUS activity in a T1 generation transgenic subterranean clover plant expressing the S7nc:GUS construct

Source of Tissue	Leaf	Petiole	Stem
Top - [folded leaf; #1 leaf position]	1	1.9	2.0
Middle [#8 leaf position]	1.6	5.8	22.0
Bottom [#17 leaf position]	4.0	4.8	12.6

Plants were 2 - 3 months old when assayed.

Results show differential expression in different tissues.

TABLE 15

Transient expression of GUS in soybean leaves directed by a SCSV promoter	
Constructs	GUS Expression in soybean leaves* (# spots/leaf)
S4nc:GUS:SC5Tr	25 - 35
35S:GUS:35STr	10 - 15

* Results from one experiment in which spots from 3 leaves were counted in each treatment

TABLE 16

Characterisation of GUS activity directed by MeA 3'L sequence (5.5kb version) in Transgenic *Flaveria bidentis* Plants

Constructs	GUS Expression
MeA:GUS:MeA 3'L (ME24)	High GUS in leaves High GUS in meristem Moderate GUS in stems
MeA:GUS:OCS 3'(ME20)	No GUS in leaves High GUS in meristem Moderate GUS in stems

TABLE 17

Transient expression of GUS in rice callus, soybean leaves and tobacco protoplasts showing enhancement of SCSV promoter activity by MeA 3's sequences in rice callus

Constructs	GUS Expression		
	Rice callus (Rel # spots)	Soybean leaves (Rel # spots)*	Tobacco protoplasts (Fluorescence)
S4nc: <i>GUS</i> :OCS 3'	ND ^a	ND	0.49
S4nc: <i>GUS</i> :SC5Tr	0.06	1	1.0
S4nc: <i>GUS</i> :MeA 3'S	1	1	1.1

ND Not done

* Average number of spots from 3 leaves in one experiment

TABLE 18

Selection of putative transgenic tobacco plants transformed with Kanamycin resistance gene driven by 35S or S4nc promoter.

Selection Criteria	Constructs	% Kanamycin resistant
npt II dot Blot	35S:npt II:35STR	(1/3)* 33%
	S4nc:npt II:SC3Tr	(7/16) 43%
Kanamycin selection in rooting medium	35S:npt II:35STR S4nc:npt II:SC3Tr	(10/21) 48% (11/21) 52%

* Number of resistant plants in total number of plants tested.

TABLE 19
Summary of the activities of SCSV transcription regulatory elements in plant tissues

A.	SCSV promoter	Gene Expressed	Protoplasts	Activity Detected	
				Transgenic Plants	Transgenic Plants
	Seg 1	GUS, nptII	Tobacco	Tobacco	Tobacco
	Seg 2	GUS	Tobacco	Tobacco	Tobacco
	Seg 3	GUS	Not done	Tobacco	Tobacco
	Seg 4	GUS	Tobacco	Tobacco, potato	Tobacco, potato
	Seg 5	GUS	Tobacco, subclover	Tobacco	Tobacco
	Seg 6	None	Not done	Not done*	Not done*
	Seg 7	GUS, nptII	Tobacco, subclover	Tobacco, subclover, cotton	Tobacco, subclover, cotton

B.	SCSV Terminator	Gene Expressed	Protoplasts	Activity Detected	
				Transgenic Plants	Transgenic Plants
	SC3Tr	GUS, nptII	Tobacco	Tobacco	Tobacco
	SC5Tr	GUS	Tobacco	Not done	Not done

* Sequence used probably insufficient to be active. Additional DNA sequence may be required as shown in segment 2.

BIBLIOGRAPHY

- [0087] An, G. (1986). Development of plant promoter expression vectors and their use for analysis of differential activity of nopaline synthase promoter in transformed cells. *Plant Physiol.* 81, 86-91.
- 5 [0088] An, G., Watson, B.D., Stachel, S., Gordon, M.P. and Nester, E.W. (1985). New cloning vehicles for transformation of higher plants. *EMBO J.* 4, 277-284.
- [0089] Benfey, P.N. and Chua, N.-H. (1990). The cauliflower mosaic virus 35S promoter: combinatorial regulation of transcription in plants. *Science* 250, 959-966.
- 10 [0090] Burns, T.M., Harding, R.M., Hafner, G., Beetham, P. and Dale, J.L. (1993). Single-stranded DNA genome organisation of banana bunchy top virus. IXth International Congress of Virology, Glasgow, Abstract W62-8.
- [0091] Chitty, J.A., Burbank, R.T., Marchall, J.S., Chen, Z. and Taylor, W.C., Genetic Transformation of the C⁴ Plant, *Flaveria bidentis*, *The Plant Journal* 6: 949-956, 1994.
- [0092] Chu, P., Boevink, P., Surin, B., Larkin, P., Keese, P. and Waterhouse, P. (1994). Non-germinated single stranded DNA plant viruses. In "Pathogenesis and host-parasite specificity in plant diseases: Vol III. Viruses and Viroids".
- 15 Pergamon Press.
- [0093] Chu, P.W.G. and Helms, K. (1988). Novel virus-like particles containing circular single-stranded DNA associated with subterranean clover stunt disease. *Virology* 167, 38-49.
- [0094] Chu, P.W.G., Keese, P., Qiu, B.S., Waterhouse, P.M. and Gerlach, W.L. (1993a). Putative full-length clones of the genomic DNA segments of subterranean clover stunt virus and identification of the segment coding for the viral coat protein. *Virus Research* 27, 161-171.
- 20 [0095] Chu, P.W.G., Qiu, B.S., Li, Z-y and Larkin, P. (1993b). Replication of subterranean clover stunt virus in pea and subterranean clover protoplasts. *Virus Research* 27, 173-183.
- [0096] Christensen, A.H., Sharrock, R.A. and Quail, P.H. (1992). Maize polyubiquitin genes: structure, thermal perturbation of expression and transcript splicing, and promoter activity following transfer to protoplasts by electroporation.
- 25 *Plant Mol. Biol.* 18, 675-689.
- [0097] Cousin, Y.L., Lyons, B.R. and Llewellyn, D.J. (1991). Transformation of an Australian cotton cultivar: prospects for cotton improvement through genetic engineering. *Aus. J. Pl. Physiol.* 18, 481-494.
- [0098] Craig, S., (1992) The GUS Reporter Gene - Application to light and transmission electron microscopy. In *GUS protocols: using the GUS gene as a reporter of gene expression*. S.R. Gallagher, Ed. Academic Press, Inc., Page 115.
- 30 [0099] Das, A. (1993). Control of transcription termination by RNA-binding proteins. *Ann. Rev. Biochem.* 62, 893-930.
- [0100] de Carvalho, F., Gheysen, G., Kushnir, S., Van Montagu, M., Inze, D. and Castresana, C. (1992). Suppression of β -1,3-glucanase transgene expression in homozygous plants. *The EMBO J.* 11, 2595-2602.
- [0101] Depicker, A., Satchel, S., Dhaese, P., Zambryski, P. and Goodman, H. (1982). Nopaline synthase: transcript mapping and DNA sequence. *J.Mol. Appl. Genet.* 1, 561-575.
- 35 [0102] Del Sal, G., Manfioletti, G. and Schnider, C. (1989). The CTAB-DNA precipitation method: a common mini-scale preparation of template DNA from pagemids, phages or plasmids suitable for sequencing. *Biotechniques* 7, 514-518.
- [0103] Devereaux, J., Haeberli, P. and Smithies, O. (1984). A comprehensive set of sequence analysis programs for the VAX. *Nucleic acids Res.* 12, 387-395.
- 40 [0104] Ditta, G., Stanfield, S., Corbin, D. and Helsinki, D.R. (1980). Broad host range DNA cloning system for gram-negative bacteria: construction of a gene bank of *Rhizobium meliloti*. *Proc. Natl. Acad. Sci. USA* 77, 7347-7351.
- [0105] Dolferus, R., Jacobs, M., Peacock, J.W., and Dennis, L.S. (1994). Differential interactions of promoter elements in stress responses of the *Arabidopsis Adh* Gene. *Plant Physiol.* 105, 1075-1087.
- [0106] Ellis, J.G., Llewellyn, D.J., Dennis, E.S. and Peacock, W.J. (1987). Maize *Adh-1* promoter sequences control anaerobic regulation: addition of upstream promoter elements from constitutive genes is necessary for expression in tobacco. *EMBO J.* 6, 11-16.
- 45 [0107] Gil, A. and Proudfoot, N.J. (1984). *Nature* 312, 473-474.
- [0108] Gil, A. and Proudfoot, N.J. (1984). A sequence downstream of AAUAAA is required for rabbit β -globin mRNA 3'-end formation.
- 50 [0109] Gleave, A.P. (1992). A versatile binary vector system with a T-DNA organisational structure conducive to efficient integration of cloned DNA into the plant genome. *Plant Molecular Biology* 20, 1203-1207.
- [0110] Harding, R.M., Burns, T.M. and Dale, J.L. (1991). Virus-like particles associated with banana bunchy top disease contain small single-stranded DNA. *J. Gen. Virol.* 72, 225-230.
- [0111] Harding, R.M., Burn, T.M., Hafner, G., Dietzgen, R.G. and Dale, J.L. (1993). Nucleotide sequence of one component of the banana bunchy top virus genome contains a putative replicase gene. *J. Gen. Virology* 74, 323-328.
- 55 [0112] Hatch, M.D. (1987) C₄ photosynthesis: A unique blend of modified biochemistry, anatomy and ultrastructure. *Biochim. Biophys. Acta* 895:81-106.
- [0113] Higgins, T.J.V. and Spencer, D. (1991). The expression of a chimeric cauliflower mosaic virus (CaMV) 35S-

pea vicilin gene in tobacco. *Plant Sci.* 74, 89-98.

[0114] Hoekema, A., Hirsch, P.R., Hooykaas, P.J.J. and Schilperoott, R.A. (1983). A binary plant vector strategy based on separation of vir- and T-region of the *Agrobacterium tumefaciens* Ti-plasmid. *Nature* 303, 179-180.

[0115] Isogai, M., Sano, Y. and Kojima, M. (1992). Identification of the unique DNA species in the milk vetch dwarf virus-infected leaves. *Ann. Phytopath. Soc. Japan* 58, 631-632, Abstract.

[0116] Jacobsen-Lyon, K., Jesen, E.O., Jorgensen, J-E., Marcker, K.A., Peacock, W.J. and Dennis, E.S. (1995). Symbiotic and nonsymbiotic hemoglobin genes of *Casuring glauca*. *Plant Cell* 7, 213-223.

[0117] Janssen, B.J. and Gardner, R.C. (1989). Localised transient expression of GUS i leaf discs following co-cultivation with *Agrobacterium*. *Plant Mol. Biol.* 14, 61-72.

[0118] Jefferson, R.A., Kavanagh, T.A. and Bevan, M.W. (1987). GUS fusions: b-glucuronidase as a sensitive and versatile gene fusion marker in higher plants. *EMBO J.* 6, 3901-3907.

[0119] Joshi, C.P. (1987). Putative polyadenylation signals in nuclear genes of higher plants: a compilation and analysis. *Nucleic Acids Research.* 15, 9627-9640.

[0120] Katul, L., Vetten, H.J., Maiss, E., Makkouk, K.M. Lesemann, D.-E. and Casper, R. (1993). Characterisation and serology of virus-like particles associated with faba bean necrotic yellows. *Ann. Appl. Biol.* 123, 629-647.

[0121] Khan, M.R.I., Tabe, L.M., Heath, L.C., Spencer, D. and Higgins, T.J.V. (1994). *Agrobacterium*-mediated transformation of subterranean clover (*Trifolium subterraneum* L.). *Plant Physiol* 105, 81-88.

[0122] Kirschman, J.A. and Cramer, J.H. (1988). Two new tools: multi-purpose cloning vectors carry kanamycin or spectinomycin/streptomycin resistance markers. *Gene* 58, 163-165.

[0123] Last, D.I., Brettell, R.I.S., Chaudhury, A.M., Chamberlain, D.A., Larkin, P.J., Marsh, E.L., Peacock, J.W. and Dennis, E.S. (1991). pEmu: an improved promoter for gene expression in cereal cells. *Theor Appl Genet* 81, 581-588.

[0124] Lazo, G.R., Stein, P.A. and Ludwig, R.A. (1991). A DNA transformation-competent *Arabidopsis* genomic library in *Agrobacterium*. *Biotechnol.* 9, 963-967.

[0125] Linn, F., Heidmann, I., Saedler, H. and Meyer, P. (1990). Epigenetic changes in the expression of the maize Z1 gene in *Petunia hybrida*: Role of numbers of integrated gene copies and state of methylation. *Mol. Gen. Genet.* 222, 329-336.

[0126] McDonnell, R.E., Clark, R.D., Smith, W.A. and Hinchee, M.A. (1987). A simplified method for the detection of neomycin phosphotransferase II activity in transformed plant tissues. *Plant Mol. Biol. Rep.* 5, 380-386.

[0127] Matzke, M.A. and Matzke, A.J.M. (1991). Differential inactivation and methylation of a transgene in plants by two suppressor loci containing homologous sequences. *Plant Mol. Biol.* 16, 821-830.

[0128] Messing, J., Geraghty, D., Heidecker, G., Hu, N-T., Kridl, J. and Rubenstein, I. (1983). Plant gene structure. In: "Genetic engineering of plants. An agricultural perspective." Kosuge, T., Meredith, C.P. and Hollaender, A. (eds). Plenum Press, New York. pp 211-277.

[0129] Nagel, R., Elliot, A., Masel, A., Birch., R.G. and Manners, J.M. (1990). Electroporation of binary Ti plasmid vector into *Agrobacterium tumefaciens* and *Agrobacterium rhizogenes*. *FEMS Microbiology Letters* 67, 325-328.

[0130] Odell, J.T., Nagy, F. and Chua, N.-H. (1985). Identification of DNA sequences required for activity of cauliflower mosaic virus 35S promoter. *Nature* 313, 810.

[0131] Pietrzak, M., Shillito, RD., Hohn, T. and Potrykus, I. (1986). Expression in plants of two bacterial antibiotic resistance genes after protoplast transformation with a new plant expression vector. *Nucleic Acids Res.* 14, 5857-5868.

[0132] Richardson, J.P. (1993). Transcription termination. *Critical Review in Biochem. and Mol. Biol.* 28, 1-30.

[0133] Rhode, W., Randles, J.W., Langridge, P. and Hanold, D. (1990). Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus. *Virology* 176, 648-651.

[0134] Rothnie, H.M., Reid, J. and Hohn, T. (1994). The contribution of AAUAAA and the upstream element UUUGUA to the efficiency of mRNA 3'-end formation in plants. *EMBO J.* 13, 2200-2210.

[0135] Sambrook, J., Fritsch, E.F. and Maniatis, T. (1989). *Molecular cloning: a laboratory manual*. 2nd ed., Cold Spring Harbor Laboratory Press, New York.

[0136] Sanger, F., Nicklen, S. and Coulson, A.R. (1977). DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. Sci. USA* 74, 5463-5467.

[0137] Sano, Y., Isogai, M., Satoh, S. and Kojima, M. (1993). Small virus-like particles containing single-stranded DNAs associated with milk vetch dwarf disease in Japan. 6th Int. Cong. of Plant Path., Montreal, Canada, July 28 - August 6, 1993. Abs. 17.1.27.

[0138] Scheid, O.M., Paszkowski, J. and Potrykus, I. (1991). Reversible inactivation of a transgene in *Arabidopsis thaliana*. *Mol. Gen. Genet.* 228, 104-112.

[0139] Schmulling, T., Schell, J. and Spena, A. (1989). Promoters of the rolA, B, and C genes of *Agrobacterium rhizogenes* are differentially regulated in plants. *Plant Cell* 1, 665-670.

[0140] Sugaya, S., Hayakawa, K., Handa, T. and Uchimiya, H. (1989). Cell-specific expression of the rolC gene of the TL-DNA of Ri plasmid in transgenic tobacco plants. *Plant Cell Physiol.* 30, 649-653.

[0141] Taylor, B.H. and Larkin, P.J. (1988). Analysis of electroporation efficiency in plant protoplasts. *Aust. J. Biotech.*

1, 52-57.

[0142] Thomas, J.E. and Dietzgen, R.G. (1991). Purification, characterization and serological detection of virus-like particles associated with banana bunchy top disease in Australia. J. Gen. Virol. 72, 217-224.

[0143] Wenzler, H., Mignery, G., May, G. and Park, W. (1989). A rapid and efficient transformation method for the production of large numbers of transgenic potato plants. Plant Science 63, 79-85.

[0144] Zheng, Z., Hayashimoto, A., Li, Z. and Murai, N. (1991). Hygromycin resistance gene cassette for vector construction and selection of transformed rice protoplasts. Plant Physiol. 97, 832-835.

SEQUENCE LISTING

[0145]

(1) GENERAL INFORMATION:

(i) APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

(ii) TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: MELBOURNE

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(E) COUNTRY: AUSTRALIA

(F) ZIP: 3000

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: AU PROVISIONAL

(B) FILING DATE: 07-NOV-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PM7770/94

(B) FILING DATE: 30-AUG-1994

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1001 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TAGTATTACC CCCGTGCCGG GATCAGAGAC ATTTGACCAA TAGTTGACTA GTATAATAGC    60
CCTTGGATTA AATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT    120
GAACGAATCT GACGGAAGAG CGTTCACACT TAGATCTAGT TAGCGTACTT AGTACGCGTT    180
GTCTTGGGTC TATAAATAGA GTGCTTCTGA ACAGATTGTT CAGAATTTCA TAGCGAGATG    240
GATTCTGGTG ATGGTTACAA TACATACTCA TATGAAGAAG GTGCTGGAGA TCGAAGAAG    300
GAAGTTTAT ATAAAATAGG TATTATTATG TTATGTATTG TAGGGATTGT AGTTTATGG    360
GTTTAAATTA TATTATGTTG TGCTGTTCCCT CGCTATGCTA AATCAACGAT GGACGCTTGG    420
TTATCTTCGT CTTCTATTAT GAAGAGGAAG ATGGCTTCAA GGATTACTGG TACTCCGTTT    480
GAAGAACTG GTCCTCATCG TGAAAGAAGA TGGGCTGAAA GAAGAACTGA AGCGACGAAC    540
CAGAATAATA ATGATAATGT AAATAGATTT AGTTGATATG TTGTAATTTT ATATGGATTA    600
ATGAGAATTA TTATTATTCT GTTCTTCGTC TGTGTTTTTT AAGCTTTTTC TGTGTTTTAA    660
TGGCGTCTGG AGAGAGAAAAG GAATAATTGT AAGGTAGACG ACGATGTAGT GGATTACAGT    720
TGTCTTTACT TCGCCTCGAA GAAAGACACA TTTCAAGTTG TGAGTGTAT TGCTTTTGAG    780
GAAGCTTCCT CGAAGCAGCG TATAACTTTA ATTTGAATTT GGTTTTGGCG CGTTAGTGAA    840
ATTGCGGCTG TAAACGTGTC AAGTTGTGAG TGGCTGAAAT AAGATAATAG ATATATTATT    900
ATTGTTTTAA TTTAATTCCG CGAAGCGATA TGTTAAGTGA TAAATGAAAC GAACGTTTTT    960
GATGACGTCA TATGTCTCCG TGCCTACGTC AGCACGGGGC T    1001

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 TAGTATTACC CGACCTTGCC ACACCTCCTT GGAACACTTT CTCTCTCTAG AAAGTGTGAG 60
 ACTTTCTCTC TCTAAGCTTA TATGGCTAGA AGGTACTGTT TTACATTAAA TTACGCTACT 120
 GAGATAGAGA GAGAAACATT CCTCTCCCTC TTCTCTCAAG ACGAATTAAA CTATTTCGTT 180
 10 GTCGGCGACG AAAGTGAAC TACTGGACAG AACACCTCC AGGGATTGTG ATCGTTCAAG 240
 AACAAAATTC GTCTTGGTGG ATTGAAGAAG AAATTTGGTA ATCGAGCTCA CTGGGAAATT 300
 GCGAGAGGCA GCGATTCTCA GAATCGCGAT TATTGCTGTA AAGAAACCCT AATTTCTGAA 360
 15 ATTGGGATTC CGGTCATGAA GGGTTCGAAC AAGCGGAAGA CGATGGAGAT TTATGAAGAG 420
 GATCCCGAAG AAATGCAATT GAAGGATCCA GATACTGCTC TTCGATGTAA GGCGAAGAAA 480
 20 TTGAAAGAGG AATATTGTTC CTGTTATGAT TTTCAGAAAC TCCGTCCATG GCAAATTGAG 540
 CTTACAGAGG ATTTAATGGC GGAACCAGAT GATCGGAGTA TCATCTGGGT CTATGGTTCA 600
 GACGGAGGAG AAGGAAAGAC GAGCTTCGCG AAGGAATTAA TCAGGTATGG ATGGTTTTAT 660
 25 ACAGCCGGAG GGAAGACCCA GGACGTATTA TATATGTATG CTCAAGACCC AGAGAGGAAT 720
 ATTGCGTTTG ATGTTCCAG GTGTTCTTCG GAGATGATGA ACTATCAGGC GATGGAGATG 780
 30 TTGAAGAACA GAGTTTTTGC AAGTACAAAA TATAGGCCTG TAGATCTTTG TATTAGGAAG 840
 TTAGTTCATT TAATTGTGTT TGCCAACGTG GCACCTGACC CCACGCGCAT AAGTGAGGAC 900
 AGACTTGTA TATCAATTG TTGAATAAAA GAATATATAT TATTGTTTTA ATTTAATTCC 960
 35 GCGAAGCGGT AGCCGGTCAT AACACTGTTG CCCTTGAAC ACTATATATA GCAAGGTCGG 1020
 CT 1022
 40

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 991 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGTATTACC CCCGTGCCGG GATCAGAGAC ATTTGACCAA TAGTTGACTA TGAATAATAG 60
 CCCTTGGATT AGATGACACG TGGACGCTCA GGATCTGTGA TGCTAGTGAA GCGCTTAAGC 120
 TGAACGAATC TGACGGAAGA GCGGACATAC GCACATGGAT TATGGCCAC ATGTCTAAAG 180
 TGTATCTCTT TACAGCTATA TTGATGTGAC GTAAGATGCT TTAATTCTGCC TCGAAGTAAA 240
 GTAGGAAATT GCTCGCTAAG TTATTCTTTT CTGAAAGAAA TTAATTTAAT TCTAAATTAA 300
 ATTAAATGAG TGGCTATAAA TAGATGTTTC GTCTTCGTTG TTTTACAACG AAGCTTAGAA 360
 TCTTGTGTTA ATGGCGTTAA GGTATTTCTC TCATCTTCCT GAAGAACTGA AGGAGAAGAT 420
 TATGAACGAG CACTTGAAGG AAATTAAGAA GAAGGAATTT CTAGAGAATG TAATTAAAGC 480
 TCGTGTGCT GTGTTCTGAAG GTTTAACAAA GAAGGAGTCT GTTGAAGAAG ACGACATACT 540
 ACGCTTCTCT GGGTTTCTGG AAGGTCTGTC TGCATATTAT GCAGAGGCGA CGAAGAAGAA 600
 GTGTTTAGTT AGATGGAAGA AGAGCGTTGC AATAAATCTG AAATGGAGAG TTATGGAGGA 660
 GATGCATTAC AAGCTTTATG GATTTCGAGA CATGGAAGAT TTATATTATT CAGAGTTAGG 720
 GTTTCCTAAT TACGGTGAAG ACGATGTAGC TTATCACCAT GGTGCAATTG TAAATTGTAA 780
 GCAATTAGAA GTTGTATTG ATGATTAGG TATTGAGTTT ATGTCTATTG TAATTGATAG 840
 AGGTTCTATT AAGATAGAAT TATGAGATGT AATTGTGATT AATGAATAAA GAGTTGTTAT 900
 TATTCTTTGA ATTACTCCGC GAAGCGGTGT GTTATGTTTT TGTGAGAGAC ATATGACGTC 960
 ATATGTCTCG CCGACAGGCT GGCACGGGGC T 991

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAGTATTACC CCGTGCCGGG ATCAGAGACA TTTGACTAAA TGTTGACTTG GAATAATAGC 60
 CCTTGATTGA GATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT 120
 GAACGAATCT GACGGAAGAG CGGACAAACG CACATGGACT ATGGCCCACT GCTTTATTAA 180
 AGAAGTGAAT GACAGCTGTC TTTGCTTCAA GACGAAGTAA AGAATAGTGG AAAACGCGTA 240
 AAGAATAAGC GTACTCAGTA CGCTTCGTGG CTTTATAAAT AGTGCTTCGT CTTATTCTTC 300
 GTTGTATCAT CAACGAAGAA GTTAAGCTTT GTTCTGCGTT TTAATGGCGG ACTGGTTTCA 360
 CAGTGCGCTT AAGACATGTA CTCATGTCTG TGATTTTTCA GATATTAAGG CGTCTTCACA 420
 ACAGGATTTC TTCTGTTGTG ATAGTATGCG AGGTAAATTA TCTGAACCTA GGAAGGTGTT 480
 GTTAGTTAGT TGTTTTGTAA GTTTTACTGG TAGTTTTTAT GGAAGTAATA GGAATGTTAG 540
 AGGTCAAGTT CAGTTGGGTA TGCAGCAAGA TGATGGCGTT GTTCGTCCAA TAGGATATAT 600
 TCCTATTGGG GGTTATTTGT ATCATGATGA TTATGGATAT TATCAAGGAG AGAAGACGTT 660
 CAATCTGGAC ATCGAGTCAG ATTATCTGAA GCCTGATGAA GATTTTTGGA AGAGATTTAC 720
 AATTAATATT GTAAATGATA AAGGATTAGA TGATAGGTGT GATGTAAAT GTTATGTAGT 780
 TCATACGATG CGTATTAAGG TGTAATTGTT ATTATCAATA AAAGAATTTT TATTGTTATT 840
 GTGTTATTTG GTAATTTATG CTTATAAGTA ATTCTATGAT TAATTGTGAA TTAATAAGAC 900
 TAATGAGGAT AATAATTGAA TTTGATTAAA TTAAGTCTGC GAAGCTATAT GTCTTTCACG 960
 TGAGAGTCAC GTGATGTCTC CGCGACAGGC TGGCACGGGG CT 1002

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAGTATTACC CCGTGCCGGG GTCAGAGACA TTTGACTAAA TATTGACTTG GAATAATAGC 60
 CCTTGGATTA GATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT 120
 5 GAACGAATCT GACGGAAGAG CGTCATGGTC CACATGTCTA AAGAATAATG CTTTACAGCT 180
 GTATTGATTT GACTTTACGC GCTTTACTTT AATTGCTTTA AGTAAAGTAA GATGCTTTAC 240
 10 TTTGCTCGCG ACGAAGCAAA GTGATTGTAG CTGCAGAAAT TGATGCTTTA ATTACCGGGT 300
 AACACGGTTT GATTGTGGGT ATAAATATGT TCTGTTTCGTT TTCTTCGTTG TCATTTTACA 360
 ACGAAGATGG TTGCTGTTTCG ATGGGGAAGA AAGGGTCTGA GGTCTCAAAG GAGAAAATAT 420
 15 TCGCGAATTG CTTACAAACC TCCTTCGTCT AAGGTTGTAA GTCATGTGGA GTCTGTTCTG 480
 AATAAGAGAG ATGTTACTGG AGCGGAGGTT AAGCCATTCG CTGATGGTTC AAGGTATAGT 540
 20 ATGAAGAAGG TAATGTTGAT TGCAACATTA ACTATGGCTC CTGGAGAATT AGTTAATTAT 600
 CTTATTGTGA AGAGTAATTC GCCTATTGCG AATTGGAGTT CGTCTTTCAG TAATCCTTCG 660
 TTGATGGTGA AAGAGTCTGT TCAAGATACA GTTACGATTG TTGGAGGAGG AAAGCTTGAG 720
 25 TCTTCTGGTA CTGCTGGTAA AGATGTA ACT AAGTCTTTTA GGAAGTTTGT TAAGCTGGGT 780
 TCAGGTATTA GTCAGACCCA GCATTTGTAT TTAATTATTT ATTCCAGTGA TGCGATGAAG 840
 ATCACACTGG AGACGAGAAT GTATATTGAT GTATAATTGT GATGATTAAT GAATAAAGAG 900
 30 TTGTTTTTAT TCTTTGAATT ACTCCGCGAA GCGGTGTGTT ATGTTTTTGT TGGAGACATA 960
 TGACGTCATA TGTCTCCGCG ACAGGCTGGC ACGGGGCT 998
 35

(2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55

CAGTATTACC GCACCTCGCT TACCCTCCTC GCTTCCCTGG GCCCACTATG CCTACTAGAC 60
 5 AAAGCACTAG TTGGGTGTTC ACACTTAACT TTGAGGGCGA AATTCCTATT TTGCCCTTTA 120
 ATGAAAGCGT TCAGTACGCT TGTGGCAGC ATGAGAGAGT GGGACACGAT CATTTACAGG 180
 GATTTATACA ATTTAAATCC CGCAACACTA CATTGCGTCA GGCTAAGTAT ATTTTAAATG 240
 10 GACTGAATCC TCATCTGGAA ATTGCTAGGG ATGTAGAGAA GCGCAATTG TACGCGATGA 300
 AGGAAGATAG TAGAGTAGCT GGTCCCTGGG AGTATGGGTT GTTTATTAAG AGAGGATCGC 360
 15 ATAAGCGTAA GCTGATGGAG AGATTTGAAG AAGATGGAGA AGAGATGAAA ATTGCTGATC 420
 CCTCTCTCTA TAGGCGTTGT CTATCAAGGA AGATGGCTGA AGAACAACGT TGTTCTTCTG 480
 AGTGGAATTA TGACTTACGC CTTGGCAAG AAGAAGTGAT GCATTTGTTA GAGGAAGAAC 540
 20 CAGATTATAG AACGATAATC TGGGTGTATG GACCTGCTGG TAATGAAGGC AAATCTACAT 600
 TTGCAAGACA TCTGTCATTG AAAGATGGTT GGGGTTATCT GCCTGGAGGA AAGACACAAG 660
 25 ATATGATGCA TCTTGTGACT GCTGAGCCTA AGAATAATTG GGTATTTGAC ATACCCAGAG 720
 TTAGTTCAGA GTATGTGAAT TATGGTGTA TAGAACAGGT TAAGAATAGG GTAATGGTGA 780
 AACTAAGTA TGAGCCATGT GTAATGCGGG ATGATAATCA TCCTGTTTAT GTAATTGTGT 840
 30 TTGCAAATGT ACTCCAGAT TTGGGAAAAT TAAGTGAAGA TAGAATAAAA TTAATTCGTT 900
 GTTGAAAAC CTGCGAAGGC AGAAGTTATA AAAAAAATGT GTTTTGAGAG AAGTCCCACA 960
 35 TCGGGTAGTT CGCGAAACAG GGTGAGGGAA GCGAGCAATA TAAGGCGAGG TCGGTAT 1017

(2) INFORMATION FOR SEQ ID NO:7:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

55

TAGTATTACC CCGTGCCGGG ATCAGAGACA TTTGACTAAA TATTGACTTG GAATAATAGC 60
 5 CCTTGGATTA GATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT 120
 GAACGAATCT GACGGAAGAG CGGACATACG CACATGGATT ATGGCCCACA TGTCTAAAGT 180
 GTATCTCTTT ACAGCTATAT TGATGTGACG TAAGATGCTT TACTTCGCTT CGAAGTAAAG 240
 10 TAGGAAATTG CTCGCTAAGT TATTCTTTTC TGAAAGAAAT TAATTTAATT CTAATTAAAT 300
 TAAATGAGTG GCTATAAATA GTGTCGATGC TGCCTCACAT CGTATTCTTC TTCGCATCGT 360
 15 CTGTTCTGGT TTTAAGCGAT GGTCAGTTTT AGTTTTCTTG AGATATACGA TGTGAGCGAC 420
 GATGTTCTTG TAAGCGATAG CAGAAGAAGT GTAGCTGTTG AGGTCGAAGA GAAGGTTCAA 480
 GTGATTAACG TGAAGGTACT GAGGTTGATT GAAGCTGTTG ATGAAGATAG AGTTGGAGTG 540
 20 AAGGTTATGT TTCGTCTGTG TTACAGATAC AGACGAGAAC TGAAGATTAC GTTGTTGGGT 600
 TGTAAGATGG AGCTATGGAC TTCGTTGAAG TCTTCAGSCA AGTATTCAGT TCAATCTTTG 660
 25 TTGCAGAGGA AGCTTAATGG TATATGTGTT AGTAATTACT GTATAGGTAT TGATATGTTT 720
 GTAAGTAATG TTAAAGAGTT GATTAATAGA TGTAATGGA TTACATCTGT TCAAGGTGTT 780
 AATCCTATAT GTTGTTTGTA TCATATGGAC GAAGAGTAAT TAATAGTAAT TATGATTAAT 840
 30 TATGAGATAA GAGTTGTTAT TAATGCTTAT GAGGAATAAA GAATGATTAA TATTGTTTAA 900
 TTTTATTCGC GAAGCGGTGT GTTATGTTTT TGTTGGAGAC ATCACGTGAC TCTCACGTGA 960
 35 TGTCTCCGCG ACAGGCTGGC ACGGGGCT 988

Claims

1. A genetic construct comprising a circovirus promoter from a circovirus which comprises a multicomponent DNA genome, said promoter being operable in a plant cell and a heterologous gene operably linked to said promoter.
2. A genetic construct according to claim 1 wherein said heterologous gene is inserted at a restriction endonuclease site downstream of said promoter.
3. A genetic construct according to claim 1 or claim 2 wherein the circovirus genome comprises more than two DNA components or segments.
4. A genetic construct according to any one of claims 1 to 3 wherein the circovirus is selected from the group consisting of subterranean clover stunt virus (SCSV), banana bunchy top virus (BBTV), milk-vetch dwarf (MDV) and fuba bean necrotic yellow virus (FBNYV).
5. A genetic construct according to claim 4 wherein the circovirus is subterranean clover stunt virus (SCSV)
6. A genetic construct according to claim 5 wherein the promoter is selected from one of the SCSV segments 1 to 7

(SEQ ID NOs: 1 to 7) or is capable of hybridizing thereto under low stringency conditions.

7. A genetic construct according to claim 6 wherein the promoter is selected from one of the SCSV segments 1, 3-5 and 7 (SEQ ID NOs. 1, 3-5 and 7) or is capable of hybridizing thereto under low stringency conditions.

8. A genetic construct according to any one of claims 1 to 7 further comprising a termination and/or polyadenylation sequence, said sequence being operably linked to said heterologous gene.

9. A genetic construct according to claim 8 wherein the termination and/or polyadenylation sequence is of SCSV origin.

10. A genetic construct according to claim 8 or 9 wherein the termination and/or polyadenylation sequence is selected from one of the SCSV segments 1 to 7 (SEQ ID NOs: 1 to 7) is capable of hybridizing thereto under low stringency conditions.

11. A genetic construct according to claim 8 wherein the termination and/or polyadenylation sequence is from the *Flaveria bidentis* MeA gene.

12. A genetic construct according to any one of claims 1 to 11 wherein the construct comprises two heterologous genes operably linked to the same or different circovirus promoters.

13. A genetic construct according to any one of claims 8 to 12 wherein the construct comprises two heterologous genes, each of which is operably linked to the same or a different circovirus promoter and a termination and/or polyadenylation sequence, which may be the same or different, operably linked to one or both of the heterologous genes.

14. A genetic construct according to any one of claims 1 to 13 wherein the or each heterologous gene is selected from:

- a) a resistance gene against plant viruses, bacteria, fungi, nematode and other pathogens;
- b) a plant virus resistance gene that confers resistance against a virus selected from alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato viruses x, y, s, m and a, cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf viruses;
- c) a gene to improve nutritional value of plants;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene;
- h) a selectable marker gene;
- i) a reporter gene;
- j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

15. A genetic construct according to claim 14 wherein:

- (i) the gene to improve nutritional value of plants is the sunflower high sulphur gene SF8;
- (ii) the insect resistance gene is BT toxin gene or proteinase inhibitor gene from *Nicotiana glauca*;
- (iii) the selectable marker gene is a gene conferring resistance to kanamycin, phosphinothricin, spectinomycin and hygromycin;
- (iv) the reporter gene is GUS, CAT and pigment genes.

16. A genetic construct comprising two or more heterologous genes operably linked to the same or different circovirus promoters operable in a plant cell, wherein each circovirus promoter is from a circovirus which comprises a multicomponent DNA genome and is operable in a plant cell.

17. A genetic construct according to claim 16 wherein the promoter is as further defined in any one of claims 3 to 7.

18. A genetic construct according to claim 16 or 17 further comprising a termination and/or polyadenylation sequence

operably linked to one or more of said heterologous genes.

19. A genetic construct according to claim 18 wherein the termination and/or polyadenylation sequence is as defined in any one of claims 9 to 11.

20. A genetic construct according to claim 18 or 19 wherein the termination and/or polyadenylation sequences are the same for each gene.

21. A genetic construct according to claim 18 or 19 wherein the termination and/or polyadenylation sequences are different for each gene.

22. A genetic construct according to any one of claims 16 to 21 wherein the heterologous genes are selected from the group consisting of:

- a) a resistance gene against a plant virus, bacterium, fungus, nematode and other pathogen;
- b) a plant virus resistance gene that confers resistance against a virus selected from alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato viruses x, y, s, m and a, cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf viruses;
- c) a gene to improve nutritional value of plants;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene;
- h) a selectable marker gene;
- i) a reporter gene;
- j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

23. A genetic construct according to claim 22 wherein:

- (i) the gene to improve nutritional value of plants is the sunflower high sulphur gene SF8;
- (ii) the insect resistance gene is BT toxin gene or proteinase inhibitor gene from *Nicotiana glauca*;
- (iii) the selectable marker gene is a gene conferring resistance to kanamycin, phosphinothricin, spectinomycin and hygromycin;
- (iv) the reporter gene is GUS, CAT and pigment genes.

24. A method of expressing a foreign gene in a plant cell, said method comprising introducing into said plant cell a genetic construct according to any one of claims 1 to 23.

25. A transgenic plant comprising the genetic construct of any one of claims 1 to 23.

Patentansprüche

1. Genkonstrukt, das einen Circoviruspromotor von einem Circovirus, das ein Mehrkomponenten-DNA-Genom umfasst, wobei der Promotor in einer Pflanzenzelle funktionsfähig ist, und ein heterologes Gen, das funktionell mit dem Promotor verbunden ist, umfasst.

2. Genkonstrukt nach Anspruch 1, wobei das heterologe Gen an einer Endonuclease-Schnittstelle stromabwärts des Promotors inseriert ist.

3. Genkonstrukt nach Anspruch 1 oder 2, wobei das Circovirusgenom mehr als zwei DNA-Komponenten oder -Segmente umfasst.

4. Genkonstrukt nach einem der Ansprüche 1 bis 3, wobei das Circovirus aus der aus Subterranean Clover Stunt Virus (SCSV), Banana Bunchy Top Virus (BBTV), Milk-Vetch Dwarf (MDV) und Faba Bean Necrotic Yellow Virus (FBNYV), bestehenden Gruppe ausgewählt ist.

5. Genkonstrukt nach Anspruch 4, wobei das Circovirus Subterranean Clover Stunt Virus (SCSV) ist.
6. Genkonstrukt nach Anspruch 5, wobei der Promotor aus einem der SCSV-Segmente 1 bis 7 (SEQ ID NO: 1 bis 7) ausgewählt ist oder mit diesem unter wenig stringenten Bedingungen hybridisieren kann.
7. Genkonstrukt nach Anspruch 6, wobei der Promotor aus einem der SCSV-Segmente 1, 3-5 und 7 (SEQ ID NO: 1, 3-5 und 7) ausgewählt ist oder mit diesem unter wenig stringenten Bedingungen hybridisieren kann.
8. Genkonstrukt nach einem der Ansprüche 1 bis 7, das ferner eine Terminations- und/oder Polyadenylierungssequenz umfasst, wobei die Sequenz mit dem heterologen Gen funktionell verbunden ist.
9. Genkonstrukt nach Anspruch 8, wobei die Terminationsund/oder Polyadenylierungssequenz von SCSV-Herkunft ist.
10. Genkonstrukt nach Anspruch 8 oder 9, wobei die Terminations- und/oder Polyadenylierungssequenz aus einem der SCSV-Segmente 1 bis 7 (SEQ ID NO: 1 bis 7) ausgewählt ist oder mit diesem unter wenig stringenten Bedingungen hybridisieren kann.
11. Genkonstrukt nach Anspruch 8, wobei die Terminationsund/oder Polyadenylierungssequenz aus dem *Flaveria bidentis*-MeA-Gen stammt.
12. Genkonstrukt nach einem der Ansprüche 1 bis 11, wobei das Konstrukt zwei heterologe Gene, die funktionell mit dem gleichen oder unterschiedlichen Circoviruspromotoren verbunden sind, umfasst.
13. Genkonstrukt nach einem der Ansprüche 8 bis 12, wobei das Konstrukt zwei heterologe Gene, von denen jedes mit dem gleichen oder einem unterschiedlichen Circoviruspromotor funktionell verbunden ist, und eine Terminations- und/oder Polyadenylierungssequenz, die gleich oder unterschiedlich sein kann, die funktionell mit einem oder beiden der heterologen Gene verbunden ist, umfasst.
14. Genkonstrukt nach einem der Ansprüche 1 bis 13, wobei das oder jedes heterologe Gen ausgewählt ist aus:
 - a) einem Resistenzgen gegenüber Pflanzenviren, Bakterien, Pilzen, Nematoden und anderen Pathogenen;
 - b) einem Pflanzenvirusresistenzgen, das Resistenz gegenüber einem Virus verleiht, das aus Alfalfa Mosaic Virus, Subterranean Clover Stunt Virus, Subterranean Clover Mottle Virus, Subterranean Clover Red Leaf Virus, Potato Leafroll Virus, Tomato Spotted Wilt Virus, Bean Yellow Mosaic Virus, White Clover Mosaic Virus, Clover Yellow Vein Virus, Potato Viruses x, y, s, m und a, Cucumber Mosaic Virus, Rice Ragged Stunt Virus und Barley Yellow Dwarf Viruses ausgewählt ist;
 - c) einem Gen zur Verbesserung des Nährwerts von Pflanzen;
 - d) einem Blähresistenzgen;
 - e) einem Antikörpergen;
 - f) einem Getreide-Thionin- und Ribosomeninaktivierungsproteingen;
 - g) einem Insektenresistenzgen;
 - h) einem Gen eines selektierbaren Markers;
 - i) einem Reporter gen;
 - j) einem Gen mit Codierung für ein regulatorisches Protein, das die Expression eines Gens in Pflanzenzellen moduliert.
15. Genkonstrukt nach Anspruch 14, wobei:
 - (i) das Gen zur Verbesserung des Nährwerts von Pflanzen das Sunflower High Sulphur-Gen SF8 ist;
 - (ii) das Insektenresistenzgen ein BT-Toxingen oder Proteinaseinhibitorgen von *Nicotiana glauca* ist;
 - (iii) das Gen eines selektierbaren Markers ein Resistenz gegenüber Kanamycin, Phosphinothricin, Spectinomycin und Hygromycin verleihendes Gen ist;
 - (iv) das Reporter gen ein GUS-, CAT- und Pigmentgen ist.
16. Genkonstrukt, das zwei oder mehrere heterologe Gene umfasst, die funktionell mit den gleichen oder unterschiedlichen in einer Pflanzenzelle funktionsfähigen Circoviruspromotoren verbunden sind, wobei jeder Circoviruspromotor aus einem Circovirus stammt, das ein Mehrkomponenten-DNA-Genom umfasst und in einer Pflanzenzelle

funktionsfähig ist.

17. Genkonstrukt nach Anspruch 16, wobei der Promotor wie ferner in einem der Ansprüche 3 bis 7 definiert ist.

18. Genkonstrukt nach Anspruch 16 oder 17, das ferner eine Terminations- und/oder Polyadenylierungssequenz, die funktionell mit einem oder mehreren der heterologen Gene verbunden ist, umfasst.

19. Genkonstrukt nach Anspruch 18, wobei die Terminationsund/oder Polyadenylierungssequenz wie in einem der Ansprüche 9 bis 11 definiert ist.

20. Genkonstrukt nach Anspruch 18 oder 19, wobei die Terminations- und/oder Polyadenylierungssequenzen für jedes Gen die gleichen sind.

21. Genkonstrukt nach Anspruch 18 oder 19, wobei die Terminations- und/oder Polyadenylierungssequenzen für jedes Gen unterschiedlich sind.

22. Genkonstrukt nach einem der Ansprüche 16 bis 21, wobei die heterologen Gene ausgewählt sind aus der Gruppe von:

- a) einem Resistenzgen gegenüber Pflanzenviren, Bakterien, Pilzen, Nematoden und anderen Pathogenen;
- b) einem Pflanzenvirusresistenzgen, das Resistenz gegenüber einem Virus verleiht, das aus Alfalfa Mosaic Virus, Subterranean Clover Stunt Virus, Subterranean Clover Mottle Virus, Subterranean Clover Red Leaf Virus, Potato Leafroll Virus, Tomato Spotted Wilt Virus, Bean Yellow Mosaic Virus, White Clover Mosaic Virus, Clover Yellow Vein Virus, Potato Viruses x, y, s, m und a, Cucumber Mosaic Virus, Rice Ragged Stunt Virus und Barley Yellow Dwarf Viruses ausgewählt ist;
- c) einem Gen zur Verbesserung des Nährwerts von Pflanzen;
- d) einem Blähresistenzgen;
- e) einem Antikörpergen;
- f) einem Getreide-Thionin- und Ribosomeninaktivierungsproteingen;
- g) einem Insektenresistenzgen;
- h) einem Gen eines selektierbaren Markers;
- i) einem Reporter-gen;
- j) einem Gen mit Codierung für ein regulatorisches Protein, das die Expression eines Gens in Pflanzenzellen moduliert.

23. Genkonstrukt nach Anspruch 22, wobei:

- (i) das Gen zur Verbesserung des Nährwerts von Pflanzen das Sunflower High Sulphur-Gen SF8 ist;
- (ii) das Insektenresistenzgen ein BT-Toxingen oder Proteinaseinhibitorgen von *Nicotiana glauca* ist;
- (iii) das Gen eines selektierbaren Markers ein Resistenz gegenüber Kanamycin, Phosphinothricin, Spectinomycin und Hygromycin verleihendes Gen ist;
- (iv) das Reporter-gen ein GUS-, CAT- und Pigmentgen ist.

24. Verfahren zur Expression eines Fremdgens in einer Pflanzenzelle, das das Einführen eines Genkonstrukts nach einem der Ansprüche 1 bis 23 in die Pflanzenzelle umfasst.

25. Transgene Pflanze, die das Genkonstrukt von einem der Ansprüche 1 bis 23 umfasst.

Revendications

1. Produit de construction génétique comprenant un promoteur de circovirus provenant d'un circovirus qui comprend un génome à ADN multicomposant, ledit promoteur pouvant fonctionner dans une cellule végétale, et un gène hétérologue fonctionnellement lié audit promoteur.

2. Produit de construction génétique selon la revendication 1, dans lequel ledit gène hétérologue est inséré au niveau d'un site pour endonucléase de restriction en aval dudit promoteur.

3. Produit de construction génétique selon la revendication 1 ou la revendication 2, dans lequel le génome de circovirus comprend plus de deux composants ou segments d'ADN.
- 5 4. Produit de construction génétique selon l'une quelconque des revendications 1 à 3, dans lequel le circovirus est choisi dans l'ensemble constitué par le virus de rabougrissement du trèfle souterrain (SCSV, pour subterranean clover stunt virus), le virus du sommet touffu du bananier (BBTV, pour banana bunchy top virus), le virus nain de l'astragale (MDV, pour milk-vetch dwarf) et le virus de la jaunisse nécrotique de la féverole (FBNYV, pour fuba bean necrotic yellow virus).
- 10 5. Produit de construction génétique selon la revendication 4, dans lequel le circovirus est le virus rabougrissement du trèfle souterrain (SCSV).
- 15 6. Produit de construction génétique selon la revendication 5, dans lequel le promoteur est choisi parmi l'un des segments 1 à 7 de SCSV (SEQ ID n° 1 à 7) ou est capable de s'hybrider avec un tel segment dans des conditions faiblement stringentes.
- 20 7. Produit de construction génétique selon la revendication 6, dans lequel le promoteur est choisi parmi l'un des segments 1, 3-5 et 7 de SCSV (SEQ ID n° 1, 3-5 et 7) ou est capable de s'hybrider avec un tel segment dans des conditions faiblement stringentes.
- 25 8. Produit de construction génétique selon l'une quelconque des revendications 1 à 7, comprenant en outre une séquence de terminaison et/ou de polyadénylation, ladite séquence étant fonctionnellement liée audit gène hétérologue.
- 30 9. Produit de construction génétique selon la revendication 8, dans lequel la séquence de terminaison et/ou de polyadénylation est d'origine SCSV.
- 35 10. Produit de construction génétique selon la revendication 8 ou 9, dans lequel la séquence de terminaison et/ou de polyadénylation est choisie parmi l'un des segments 1 à 7 de SCSV (SEQ ID n° 1 à 7) ou est capable de s'hybrider avec un tel segment dans des conditions faiblement stringentes.
- 40 11. Produit de construction génétique selon la revendication 8, dans lequel la séquence de terminaison et/ou de polyadénylation provient du gène MeA de *Flaveria bidentis*.
- 45 12. Produit de construction génétique selon l'une quelconque des revendications 1 à 11, dans lequel le produit de construction comprend deux gènes hétérologues fonctionnellement liés au même promoteur de circovirus ou à un promoteur différent de circovirus.
- 50 13. Produit de construction génétique selon l'une quelconque des revendications 8 à 12, dans lequel le produit de construction comprend deux gènes hétérologues, chacun d'eux étant fonctionnellement lié au même promoteur de circovirus ou à un promoteur différent de circovirus et une séquence de terminaison et/ou de polyadénylation, qui peut être identique ou différente, fonctionnellement liée à l'une des gènes hétérologues ou aux deux.
- 55 14. Produit de construction génétique selon l'une quelconque des revendications 1 à 13, dans lequel le ou chaque gène hétérologue est choisi parmi :
 - a) un gène de résistance à des virus de plantes, des bactéries, des champignons, des nématodes et d'autres agents pathogènes ;
 - b) un gène de résistance à un virus de plante, qui confère une résistance à un virus choisi parmi le virus de la mosaïque de la luzerne, le virus rabougrissement du trèfle souterrain, le virus de la marbrure du trèfle souterrain, le virus de la feuille rouge du trèfle souterrain, le virus de l'enroulement de la pomme de terre, le virus de la maladie bronzée de la tomate, le virus de la mosaïque jaune du haricot, le virus de la mosaïque du trèfle blanc, le virus de la jaunisse des nervures du trèfle, les virus de la pomme de terre x, y, s, m et a, le virus de la mosaïque du concombre, le virus de l'échancrure et du nanisme du riz et les virus de la jaunisse nanisante de l'orge ;
 - c) un gène destiné à améliorer la valeur nutritionnelle de plantes ;
 - d) un gène de résistance au gonflement ;
 - e) un gène d'anticorps ;

- f) un gène de protéine d'inactivation du ribosome et de thionine de céréale ;
- g) un gène de résistance à des insectes ;
- h) un gène marqueur de sélection ;
- i) un gène rapporteur ;
- j) un gène codant pour une protéine régulatrice qui module l'expression d'un gène dans des cellules végétales.

15. Produit de construction selon la revendication 14, dans laquelle :

- (i) le gène destiné à améliorer la valeur nutritionnelle de plantes est le gène de haute teneur en soufre du tournesol SF8 ;
- (ii) le gène de résistance à des insectes est le gène de toxine BT ou le gène inhibiteur de protéinase provenant de *Nicotiana glauca* ;
- (iii) le gène marqueur de sélection est un gène conférant la résistance à la kanamycine, la phosphinothricine, la spectinomycine et l'hygromycine ;
- (iv) le gène rapporteur est GUS, CAT et des gènes de pigments.

16. Produit de construction comprenant deux ou plus de deux gènes hétérologues fonctionnellement liés au même promoteur de circovirus ou à un promoteur différent de circovirus pouvant fonctionner dans une cellule végétale, chaque promoteur de circovirus provenant d'un circovirus qui comprend un génome d'ADN multicomposant et pouvant fonctionner dans une cellule végétale.

17. Produit de construction de gène selon la revendication 16, dans lequel le promoteur est en outre défini dans l'une quelconque des revendications 3 à 7.

18. Produit de construction génétique selon la revendication 16 ou 17, comprenant en outre une séquence de terminaison et/ou de polyadénylation fonctionnellement liée à un ou plusieurs desdits gènes hétérologues.

19. Produit de construction génétique selon la revendication 18, dans lequel la séquence de terminaison et/ou de polyadénylation est telle que définie dans l'une quelconque des revendications 9 à 11.

20. Produit de construction génétique selon la revendication 18 ou 19, dans lequel les séquences de terminaison et/ou de polyadénylation sont les mêmes pour chaque gène.

21. Produit de construction génétique selon la revendication 18 ou 19, dans lequel les séquences de terminaison et/ou de polyadénylation sont différentes pour chaque gène.

22. Produit de construction génétique selon l'une quelconque des revendications 16 à 21, dans lequel les gènes hétérologues sont choisis dans le groupe constitué par :

- a) un gène de résistance à un virus de plante, une bactérie, un champignon, un nématode et un autre agent pathogène ;
- b) un gène de résistance à un virus de plante, qui confère une résistance à un virus choisi parmi le virus de la mosaïque de la luzerne, le virus rabougrissement du trèfle souterrain, le virus de la marbrure du trèfle souterrain, le virus de la feuille rouge du trèfle souterrain, le virus de l'enroulement de la pomme de terre, le virus de la maladie bronzée de la tomate, le virus de la mosaïque jaune du haricot, le virus de la mosaïque du trèfle blanc, le virus de la jaunisse des nervures du trèfle, les virus de la pomme de terre x, y, s, m et a, le virus de la mosaïque du concombre, le virus de l'échancrure et du nanisme du riz et les virus de la jaunisse nanisante de l'orge ;
- c) un gène destiné à améliorer la valeur nutritionnelle de plantes ;
- d) un gène de résistance au gonflement ;
- e) un gène d'anticorps ;
- f) un gène de protéine d'inactivation du ribosome et de thionine de céréale ;
- g) un gène de résistance à des insectes ;
- h) un gène marqueur de sélection ;
- i) un gène rapporteur ;
- j) un gène codant pour une protéine régulatrice qui module l'expression d'un gène dans des cellules végétales.

23. Produit de construction génétique selon la revendication 22, dans lequel :

(i) le gène destiné à améliorer la valeur nutritionnelle de plantes est le gène de haute teneur en soufre du tournesol SF8 ;

(ii) le gène de résistance à des insectes est le gène de toxine BT ou le gène inhibiteur de protéinase provenant de *Nicotiana glauca* ;

(iii) le gène marqueur de sélection est un gène conférant la résistance à la kanamycine, la phosphinothricine, la spectinomycine et l'hygromycine ;

(iv) le gène rapporteur est GUS, CAT et des gènes de pigments.

24. Procédé d'expression d'un gène étranger dans une cellule végétale, ledit procédé comprenant l'introduction dans ladite cellule végétale d'un produit de construction génétique selon l'une quelconque des revendications 1 à 23.

25. Plante transgénique comprenant le produit de construction génétique selon l'une quelconque des revendications 1 à 23.

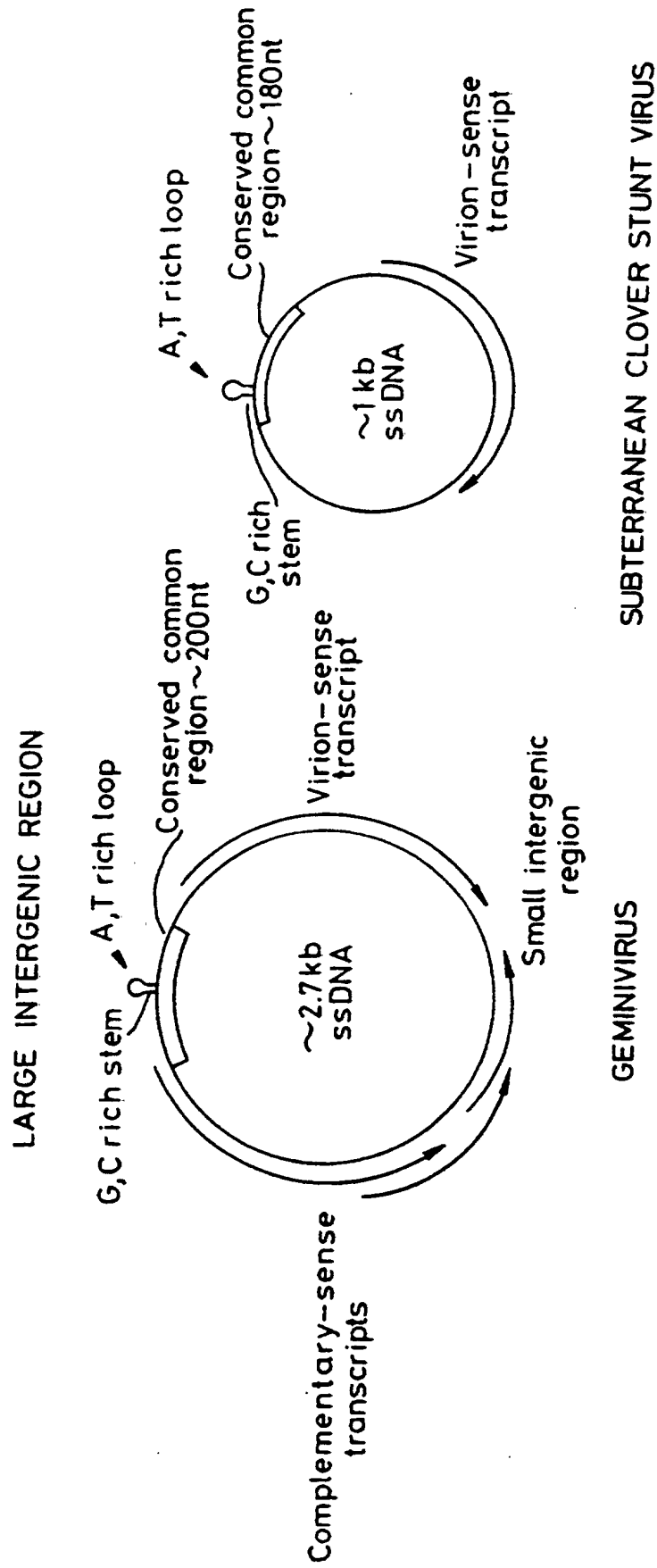


Fig.1

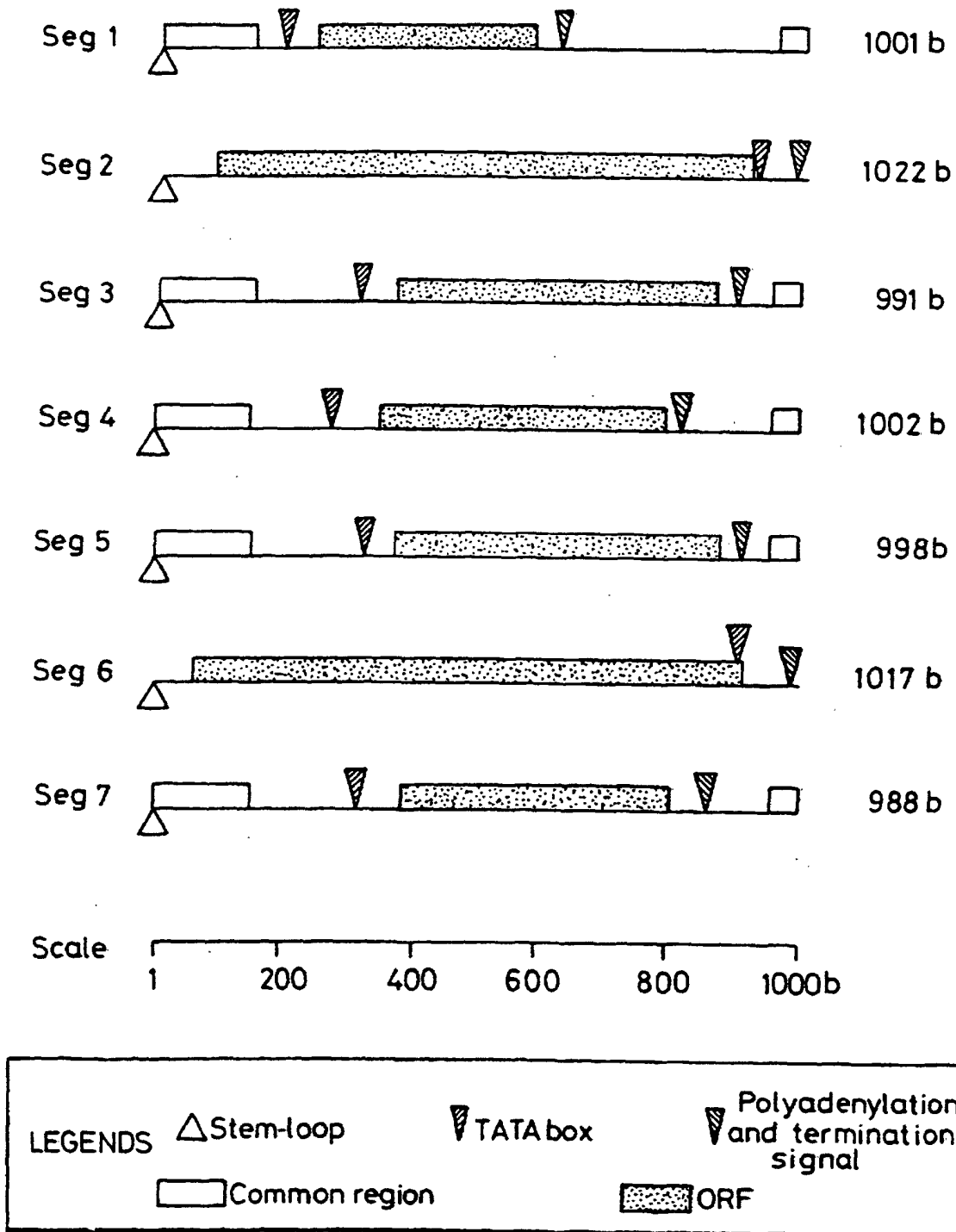


Fig. 2

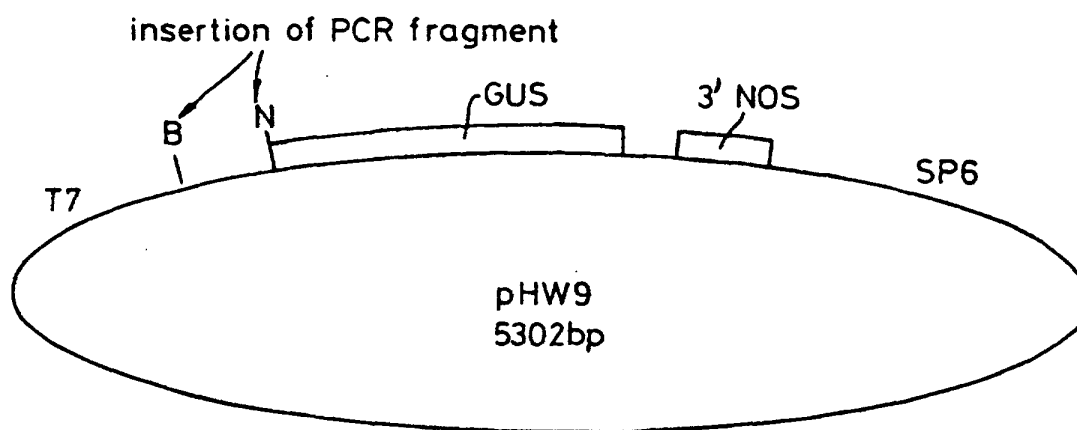
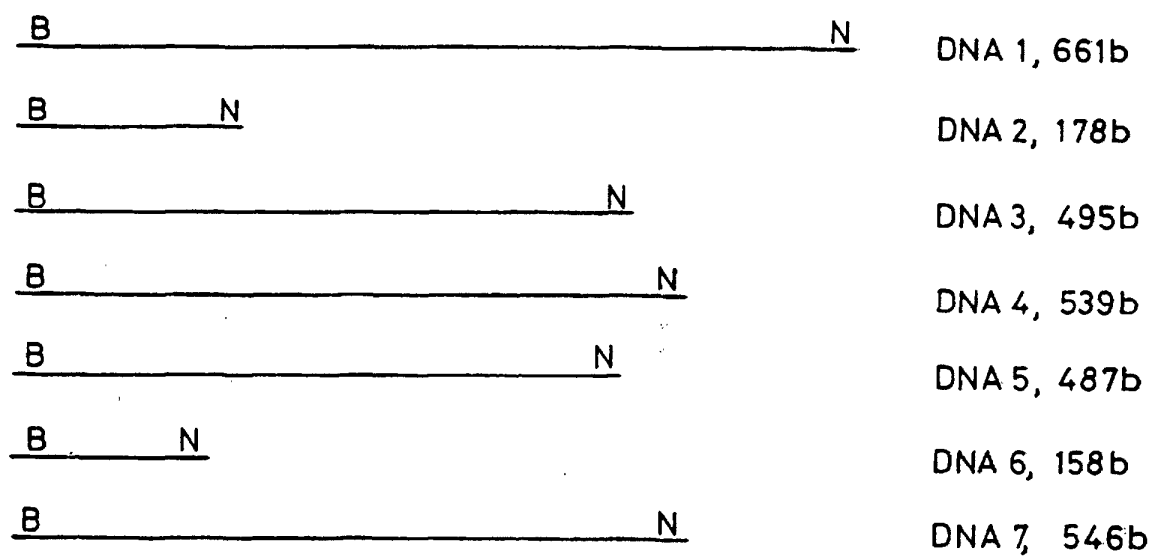
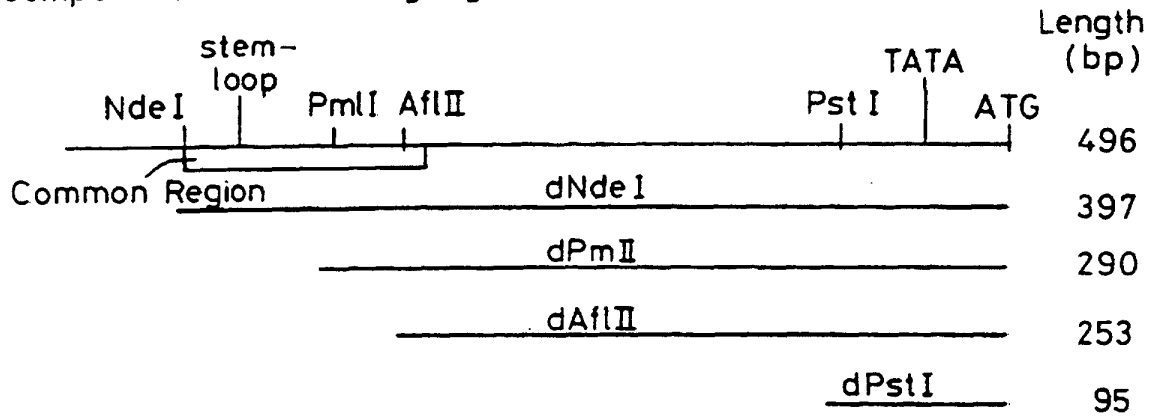


Fig. 3

Component 5 non-coding region and deletions.



Component 7 non-coding region and deletion

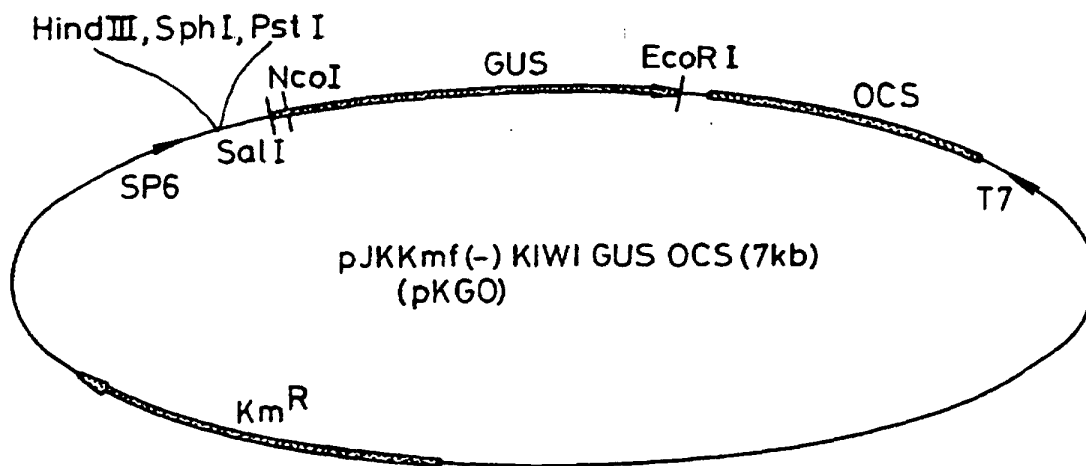
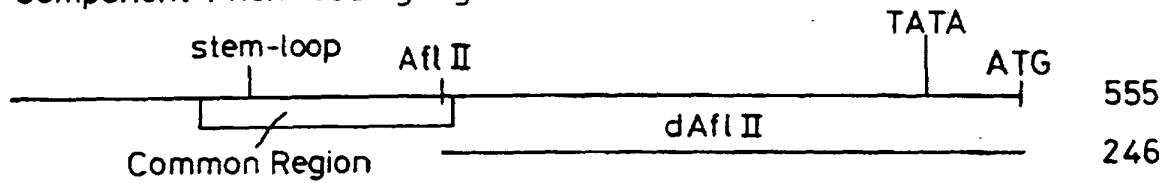


Fig.4

Plasmid pBs 150

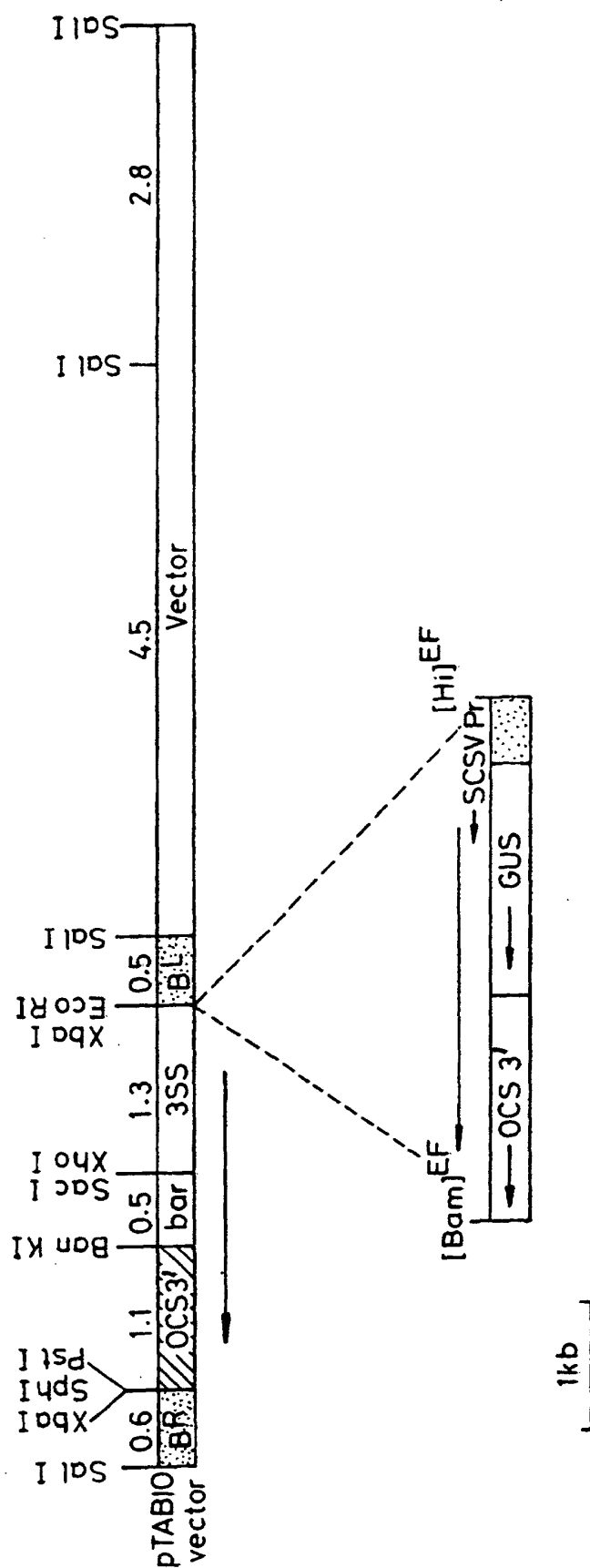


Fig. 5

COMPONENT 1

1	TAGTATTACC	CCCGTGCCGG	GATCAGAGAC
61	CCTTGGATTA	AATGACACGT	GGACGCTCAG
121	GAACGAATCT	GACGGAAGAG	CGTTCACACT
181	GTCTTGGGTC	TATAAATAGA	GTGCTTCTGA
241	GATTCTGGTG	ATGGTTACAA	TACATACTCA
301	GAAGTTTTAT	ATAAAATAGG	TATTATTATG
361	GTTTTAATTA	TATTATGTTG	TGCTGTTTCCT
421	TTATCTTCGT	CTTCTATTAT	GAAGAGGAAG
481	GAAGAAACTG	GTCCTCATCG	TGAAAGAAGA
541	CAGAATAATA	ATGATAATGT	AAATAGATTT
601	ATGAGAATTA	TTATTATTCT	GTTCTTCGTC
661	TGGCGTCTGG	AGAGAGAAAG	GAATAATTGT
721	TGTCTTTACT	TCGCCTCGAA	GAAAGACACA
781	GAAGCTTCCT	CGAAGCAGCG	TATAACTTTA
841	ATTGCGGCTG	TAAACGTGTC	AAGTTGTGAG
901	ATTGTTTTAA	TTTAATTCCG	CGAAGCGATA
961	GATGACGTCA	TATGTCTCCG	TGCCTACGTC

Fig. 6

COMPONENT 1 (cont.)

ATTTGACCAA	TAGTTGACTA	GTATAATAGC	60
GATCTGTGAT	GCTAGTGAAG	CGCTTAAGCT	120
TAGATCTAGT	TAGCGTACTT	AGTACGCGTT	180
ACAGATTGTT	CAGAATTTCA	TAGCGAGATG	240
TATGAAGAAG	GTGCTGGAGA	TGCGAAGAAG	300
TTATGTATTG	TAGGGATTGT	AGTTTTATGG	360
CGCTATGCTA	AATCAACGAT	GGACGCTTGG	420
ATGGCTTCAA	GGATTACTGG	TACTCCGTTT	480
TGGGCTGAAA	GAAGAACTGA	AGCGACGAAC	540
AGTTGATATG	TTGTAATTTT	ATATGGATTA	600
TGTGTTTTTT	AAGCTTTTTT	TGTGTTTTTAA	660
AAGGTAGACG	ACGATGTAGT	GGATTACAGT	720
TTTCAAGTTG	TGAGTGTTAT	TGCTTTTGAG	780
ATTTGAATTT	GGTTTTGGCG	CGTTAGTGAA	840
TGGCTGAAAT	AAGATAATAG	ATATATTATT	900
TGTTAAGTGA	TAAATGAAAC	GAAGCGTTTT	960
AGCACGGGGC	T		1001

Fig. 6(cont.)

COMPONENT 2

1	TAGTATTACC	CGACCTTGCC	ACACCTCCTT
61	ACTTTCTCTC	TCTAAGCTTA	TATGGCTAGA
121	GAGATAGAGA	GAGAAACATT	CCTCTCCCTC
181	GTCGGCGACG	AAACTGCAAC	TACTGGACAG
241	AACAAAATTC	GTCTTGGTGG	ATTGAAGAAG
301	GCGAGAGGCA	GCGATTCTCA	GAATCGCGAT
361	ATTGGGATTC	CGGTCATGAA	GGGTTCGAAC
421	GATCCCGAAG	AAATGCAATT	GAAGGATCCA
481	TTGAAAGAGG	AATATTGTTC	CTGTTATGAT
541	CTTCACGAGG	ATTTAATGGC	GGAACCAGAT
601	GACGGAGGAG	AAGGAAAGAC	GAGCTTCGCG
661	ACAGCCGGAG	GGAAGACCCA	GGACGTATTA
721	ATTGCGTTTG	ATGTTCCCAG	GTGTTCTTCG
781	TTGAAGAACA	GAGTTTTTGC	AAGTACAAAA
841	TTAGTTCATT	TAATTGTGTT	TGCCAACGTG
901	AGACTTGTA	TTATCAATTG	TTGAATAAAA
961	GCGAAGCGGT	AGCCGGTCAT	AACACTGTTG
1021	CT		

Fig. 6(cont.)

COMPONENT 2 (cont.)

GGAACACTTT	CTCTCTCTAG	AAAGTGTGAG	60
AGGTACTGTT	TTACATTAAA	TTACGCTACT	120
TTCTCTCAAG	ACGAATTAAA	CTATTTTCGTT	180
AAACACCTCC	AGGGATTTGT	ATCGTTCAAG	240
AAATTTGGTA	ATCGAGCTCA	CTGGGAAATT	300
TATTGCTGTA	AAGAAACCCT	AATTTCTGAA	360
AAGCGGAAGA	CGATGGAGAT	TTATGAAGAG	420
GATACTGCTC	TTCGATGTAA	GGCGAAGAAA	480
TTTCAGAAAC	TCCGTCCATG	GCAAATTGAG	540
AAGGAATTAA	TCAGGTATGG	ATGGTTTTAT	660
TATATGTATG	CTCAAGACCC	AGAGAGGAAT	720
GAGATGATGA	ACTATCAGGC	GATGGAGATG	780
TATAGGCCTG	TAGATCTTTG	TATTAGGAAG	840
GCACCTGACC	CCACGCGCAT	AAGTGAGGAC	900
GAATATATAT	TATTGTTTTA	ATTTAATTCC	960
CCCTTGGAAC	ACTATATATA	GCAAGGTCGG	1020
			1022

Fig. 6(cont.)

COMPONENT 3

1	TAGTATTACC	CCCGTGCCGG	GATCAGAGAC
61	CCCTTGGATT	AGATGACACG	TGGACGCTCA
121	TGAACGAATC	TGACGGAAGA	GCGGACATAC
181	TGTATCTCTT	TACAGCTATA	TTGATGTGAC
241	GTAGGAAATT	GCTCGCTAAG	TTATTCTTTT
301	ATTAAATGAG	TGGCTATAAA	TAGATGTTTC
361	TCTTGTGTTA	ATGGCGTTAA	GGTATTTCTC
421	TATGAACGAG	CACTTGAAGG	AAATTAAGAA
481	TGCGTGTGCT	GTGTTCGAAG	GTTTAACAAA
541	ACGCTTCTCT	GGGTTTCTGG	AAGGTCTGTC
601	GTGTTTAGTT	AGATGGAAGA	AGAGCGTTGC
661	GATGCATTAC	AAGCTTTATG	GATTTGCAGA
721	GTTTCCTAAT	TACGGTGAAG	ACGATGTAGC
781	GCAATTAGAA	GTTGTATTTG	ATGATTTAGG
841	AGGTTCTATT	AAGATAGAAT	TATGAGATGT
901	TATTCTTTGA	ATTACTCCGC	GAAGCGGTGT
961	ATATGTCTCG	CCGACAGGCT	GGCACGGGGC

Fig. 6 (cont.)

COMPONENT 3 (cont.)

ATTTGACCAA TAGTTGACTA TGAATAATAG	60
GGATCTGTGA TGCTAGTGAA GCGCTTAAGC	120
GCACATGGAT TATGGCCCAC ATGTCTAAAG	180
GTAAGATGCT TTACTTCGCC TCGAAGTAAA	240
CTGAAAGAAA TTAATTTAAT TCTAAATTAA	300
GTCTTCGTTG TTTTACAACG AAGCTTAGAA	360
TCATCTTCCT GAAGAACTGA AGGAGAAGAT	420
GAAGGAATTT CTAGAGAATG TAATTAAAGC	480
GAAGGAGTCT GTTGAAGAAG ACGACATACT	540
TGCATATTAT GCAGAGGCGA CGAAGAAGAA	600
AATAAATCTG AAATGGAGAG TTATGGAGGA	660
CATGGAAGAT TTATATTATT CAGAGTTAGG	720
TTATCACGAT GGTGCAATTG TAAATTGTAA	780
TATTGAGTTT ATGTCTATTG TAATTGATAG	840
AATTGTGATT AATGAATAAA GAGTTGTTAT	900
GTTATGTTTT TGTTGGAGAC ATATGACGTC	960
T	991

Fig. 6(cont.)

COMPONENT 4

1	TAGTATTACC	CCGTGCCGGG	ATCAGAGACA
61	CCTTGGATTA	GATGACACGT	GGACGCTCAG
121	GAACGAATCT	GACGGAAGAG	CGGACAAACG
181	AGAAGTGAAT	GACAGCTGTC	TTTGCTTCAA
241	AAGAATAAGC	GTACTCAGTA	CGCTTCGTGG
301	GTTGTATCAT	CAACGAAGAA	GTTAAGCTTT
361	CAGTGCGCTT	AAGACATGTA	CTCATGTCTG
421	ACAGGATTTC	TTCTGTTGTG	ATAGTATGCG
481	GTTAGTTAGT	TGTTTTGTAA	GTTTTACTGG
541	AGGTCAAGTT	CAGTTGGGTA	TGCAGCAAGA
601	TCCTATTGGG	GGTTATTTGT	ATCATGATGA
661	CAATCTGGAC	ATCGAGTCAG	ATTATCTGAA
721	AATTAATATT	GTAAATGATA	AAGGATTAGA
781	TCATACGATG	CGTATTAAGG	TGTAATTGTT
841	GTGTTATTTG	GTAATTTATG	CTTATAAGTA
901	TAATGAGGAT	AATAATTGAA	TTTGATTAAA
961	TGAGAGTCAC	GTGATGTCTC	CGCGACAGGC

Fig. 6(cont.)

COMPONENT 4 (cont.)

TTTGACTAAA	TGTTGACTTG	GAATAATAGC	60
GATCTGTGAT	GCTAGTGAAG	CGCTTAAGCT	120
CACATGGACT	ATGGCCCCACT	GCTTTATTAA	180
GACGAAGTAA	AGAATAGTGG	AAAACGCGTA	240
CTTTATAAAT	AGTGCTTCGT	CTTATTCTTC	300
GTTCTGCGTT	TTAATGGCGG	ACTGGTTTCA	360
TGATTTTTTCA	GATATTAAGG	CGTCTTCACA	420
AGGTAAATTA	TCTGAACCTA	GGAAGGTGTT	480
TAGTTTTTTAT	GGAAGTAATA	GGAATGTTAG	540
TGATGGCGTT	GTTCGTCCAA	TAGGATATAT	600
TTATGGATAT	TATCAAGGAG	AGAAGACGTT	660
GCCTGATGAA	GATTTTTTGA	AGAGATTTAC	720
TGATAGGTGT	GATGTAAAAT	GTTATGTAGT	780
ATTATCAATA	AAAGAATTTT	TATTGTTATT	840
ATTCTATGAT	TAATTGTGAA	TTAATAAGAC	900
TTAACTCTGC	GAAGCTATAT	GTCTTTCACG	960
TGGCACGGGG	CT		1002

Fig. 6(cont.)

COMPONENT 5

1	TAGTATTACC	CCGTGCCGGG	GTCAGAGACA
61	CCTTGGATTA	GATGACACGT	GGACGCTCAG
121	GAACGAATCT	GACGGAAGAG	CGTCATGGTC
181	GTATTGATTT	GACTTTACGC	GCTTTACTTT
241	TTTGCTCGCG	ACGAAGCAAA	GTGATTGTAG
301	AACACGGTTT	GATTGTGGGT	ATAAATATGT
361	ACGAAGATGG	TTGCTGTTCG	ATGGGGAAGA
421	TCGCGAATTG	CTTACAAACC	TCCTTCGTCT
481	AATAAGAGAG	ATGTTACTGG	AGCGGAGGTT
541	ATGAAGAAGG	TAATGTTGAT	TGCAACATTA
601	CTTATTGTGA	AGAGTAATTC	GCCTATTGCG
661	TTGATGGTGA	AAGAGTCTGT	TCAAGATACA
721	TCTTCTGGTA	CTGCTGGTAA	AGATGTAACT
781	TCAGGTATTA	GTCAGACCCA	GCATTTGTAT
841	ATCACACTGG	AGACGAGAAT	GTATATTGAT
901	TTGTTTTTAT	TCTTTGAATT	ACTCCGCGAA
961	TGACGTCATA	TGTCTCCGCG	ACAGGCTGGC

Fig. 6 (cont.)

COMPONENT 5 (cont.)

TTTGACTAAA	TATTGACTTG	GAATAATAGC	60
GATCTGTGAT	GCTAGTGAAG	CGCTTAAGCT	120
CACATGTCTA	AAGAATAATG	CTTTACAGCT	180
AATTGCTTTA	AGTAAAGTAA	GATGCTTTAC	240
CTGCAGAAAT	TGATGCTTTA	ATTACCGGGT	300
TCTGTTCGTT	TTCTTCGTTG	TCATTTTACA	360
AAGGGTCTGA	GGTCTCAAAG	GAGAAAATAT	420
AAGGTTGTAA	GTCATGTGGA	GTCTGTTCTG	480
AAGCCATTCG	CTGATGGTTC	AAGGTATAGT	540
ACTATGGCTC	CTGGAGAATT	AGTTAATTAT	600
AATTGGAGTT	CGTCTTTCAG	TAATCCTTCG	660
GTTACGATTG	TTGGAGGAGG	AAAGCTTGAG	720
AAGTCTTTTA	GGAAGTTTGT	TAAGCTGGGT	780
TTAATTATTT	ATTCCAGTGA	TGCGATGAAG	840
GTATAATTGT	GATGATTAAT	GAATAAAGAG	900
GCGGTGTGTT	ATGTTTTTGT	TGGAGACATA	960
ACGGGGCT			998

Fig. 6(cont.)

COMPONENT 6

1 CAGTATTACC GCACCTCGCT TACCCTCCTC
 61 AAAGCACTAG TTGGGTGTTC AACTTAACT
 121 ATGAAAGCGT TCAGTACGCT TGTTGGCAGC
 181 GATTTATACA ATTTAAATCC CGCAACACTA
 241 GACTGAATCC TCATCTGGAA ATTGCTAGGG
 301 AGGAAGATAG TAGAGTAGCT GGTCCCTGGG
 361 ATAAGCGTAA GCTGATGGAG AGATTTGAAG
 421 CCTCTCTCTA TAGGCGTTGT CTATCAAGGA
 481 AGTGGAATTA TGACTTACGC CCTTGGCAAG
 541 CAGATTATAG AACGATAATC TGGGTGTATG
 601 TTGCAAGACA TCTGTCATTG AAAGATGGTT
 661 ATATGATGCA TCTTGTGACT GCTGAGCCTA
 721 TTAGTTCAGA GTATGTGAAT TATGGTGTA
 781 ATACTAAGTA TGAGCCATGT GTAATGCGGG
 841 TTGCAAATGT ACTCCCAGAT TTGGGAAAAT
 901 GTTGAAAACCT CTGCGAAGGC AGAAGTTATA
 961 TCGGGTAGTT CGCGAAACAG GGTGAGGGAA

Fig. 6(cont.)

COMPONENT 6 (cont.)

GCTTCCCTGG	GCCCACTATG	CCTACTAGAC	60
TTGAGGGCGA	AATTCCTATT	TTGCCCTTTA	120
ATGAGAGAGT	GGGACACGAT	CATTTACAGG	180
CATTGCGTCA	GGCTAAGTAT	ATTTTTAATG	240
ATGTAGAGAA	GGCGCAATTG	TACGCGATGA	300
AGTATGGGTT	GTTTATTAAG	AGAGGATCGC	360
AAGATGGAGA	AGAGATGAAA	ATTGCTGATC	420
AGATGGCTGA	AGAACAACGT	TGTTCTTCTG	480
AAGAAGTGAT	GCATTTGTTA	GAGGAAGAAC	540
GACCTGCTGG	TAATGAAGGC	AAATCTACAT	600
GGGGTTATCT	GCCTGGAGGA	AAGACACAAG	660
AGAATAATTG	GGTATTTGAC	ATACCCAGAG	720
TAGAACAGGT	TAAGAATAGG	GTAATGGTGA	780
ATGATAATCA	TCCTGTTCAT	GTAATTGTGT	840
TAAGTGAAGA	TAGAATAAAA	TTAATTCGTT	900
AAAAAAATGT	GTTTTGAGAG	AAGTCCCACA	960
GCGAGCAATA	TAAGGCGAGG	TGCGTAT	1017

Fig. 6 (cont.)

COMPONENT 7

1	TAGTATTACC	CCGTGCCGGG	ATCAGAGACA
61	CCTTGGATTA	GATGACACGT	GGACGCTCAG
121	GAACGAATCT	GACGGAAGAG	CGGACATACG
181	GTATCTCTTT	ACAGCTATAT	TGATGTGACG
241	TAGGAAATTG	CTCGCTAAGT	TATTCTTTTC
301	TAAATGAGTG	GCTATAAATA	GTGTCGATGC
361	CTGTTCTGGT	TTTAAGCGAT	GGTCAGTTTT
421	GATGTTCTTG	TAAGCGATAG	CAGAAGAAGT
481	GTGATTAACG	TGAAGGTACT	GAGGTTGATT
541	AAGGTTATGT	TTCGTCTGTG	TTACAGATAC
601	TGTAAGATGG	AGCTATGGAC	TTCGTTGAAG
661	TTGCAGAGGA	AGCTTAATGG	TATATGTGTT
721	GTAAGTAATG	TTAAAGAGTT	GATTAATAGA
781	AATCCTATAT	GTTGTTTGTA	TCATATGGAC
841	TATGAGATAA	GAGTTGTTAT	TAATGCTTAT
901	TTTTATTCGC	GAAGCGGTGT	GTTATGTTTT

Fig. 6(cont.)

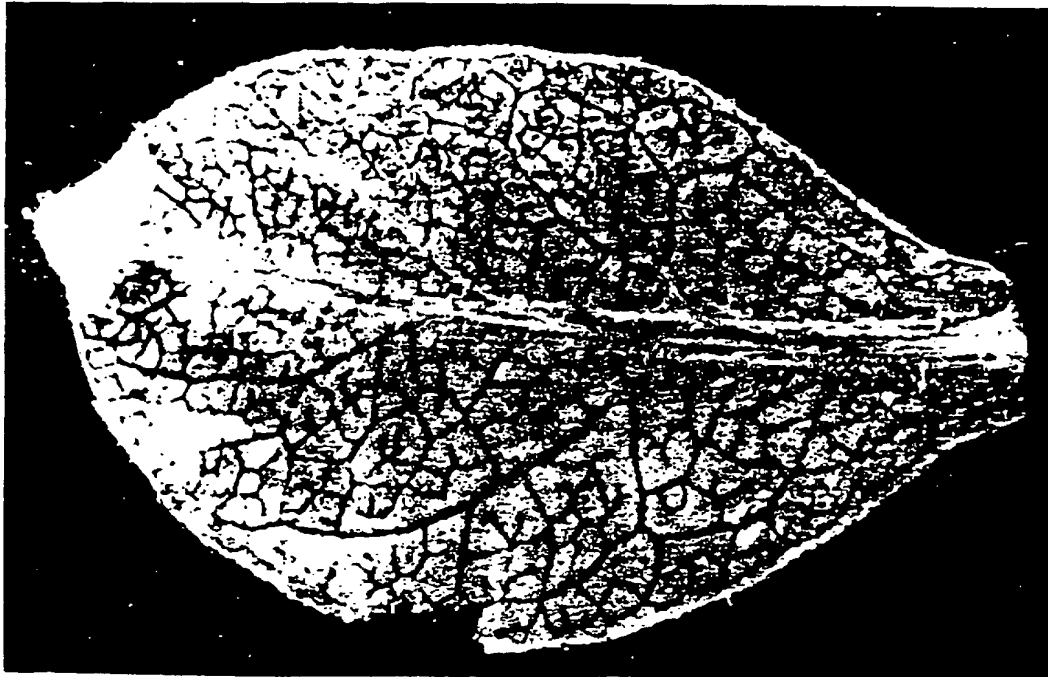
COMPONENT 7 (cont.)

TTTGACTAAA	TATTGACTTG	GAATAATAGC	60
GATCTGTGAT	GCTAGTGAAG	CGCTTAAGCT	120
CACATGGATT	ATGGCCCACA	TGTCTAAAGT	180
TAAGATGCTT	TACTTCGCTT	CGAAGTAAAG	240
TGAAAGAAAT	TAATTTAATT	CTAATTAAAT	300
TGCCTCACAT	CGTATTCTTC	TTCGCATCGT	360
AGTTTTCTTG	AGATATACGA	TGTGAGCGAC	420
GTAGCTGTTG	AGGTCGAAGA	GAAGGTTCAA	480
GAAGCTGTTG	ATGAAGATAG	AGTTGGAGTG	540
AGACGAGAAC	TGAAGATTAC	GTTGTTGGGT	600
TCTTCAGGCA	AGTATTCAGT	TCAATCTTTG	660
AGTAATTACT	GTATAGGTAT	TGATATGTTT	720
TGTAAATGGA	TTACATCTGT	TCAAGGTGTT	780
GAAGAGTAAT	TAATAGTAAT	TATGATTAAT	840
GAGGAATAAA	GAATGATTAA	TATTGTTTAA	900
TGTTGGAGAC	ATCACGTGAC	TCTCACGTGA	960
TGTCTCCGCG	ACAGGCTGGC	ACGGGGCT	988

Fig. 6 (cont.)



Subterranean Clover



Tobacco

Fig. 7

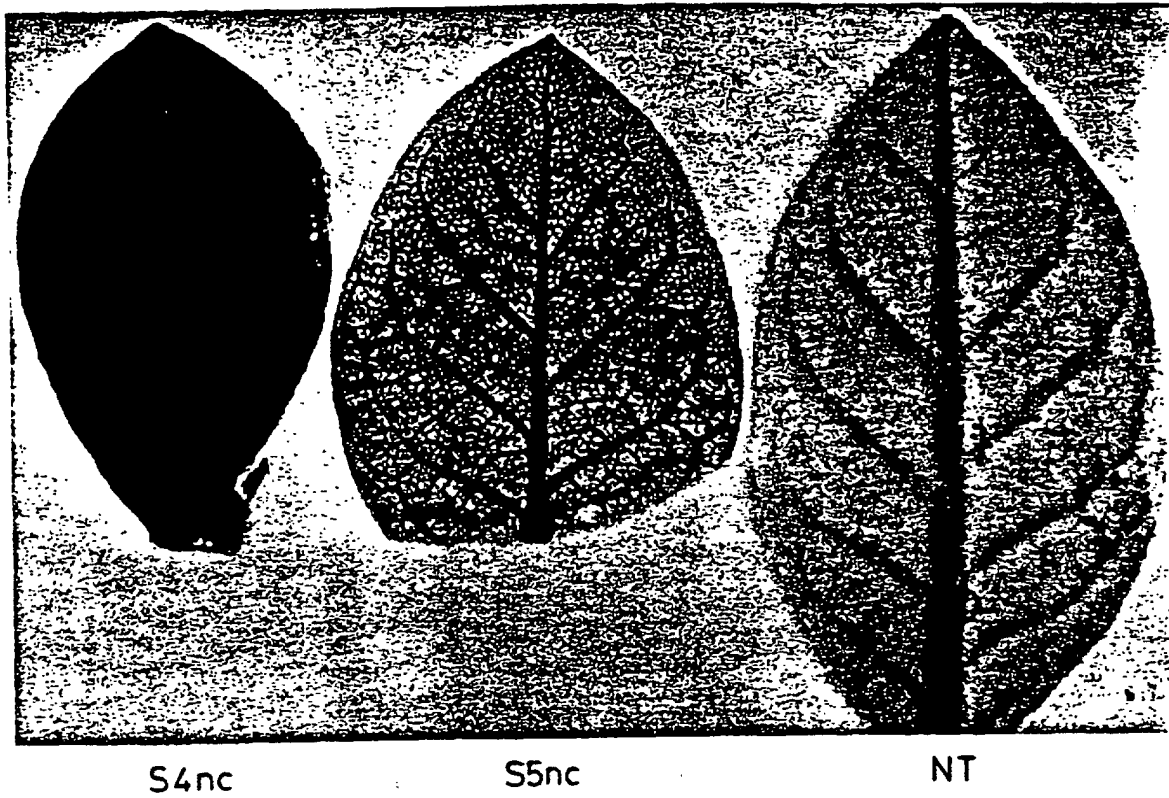


Fig. 8a

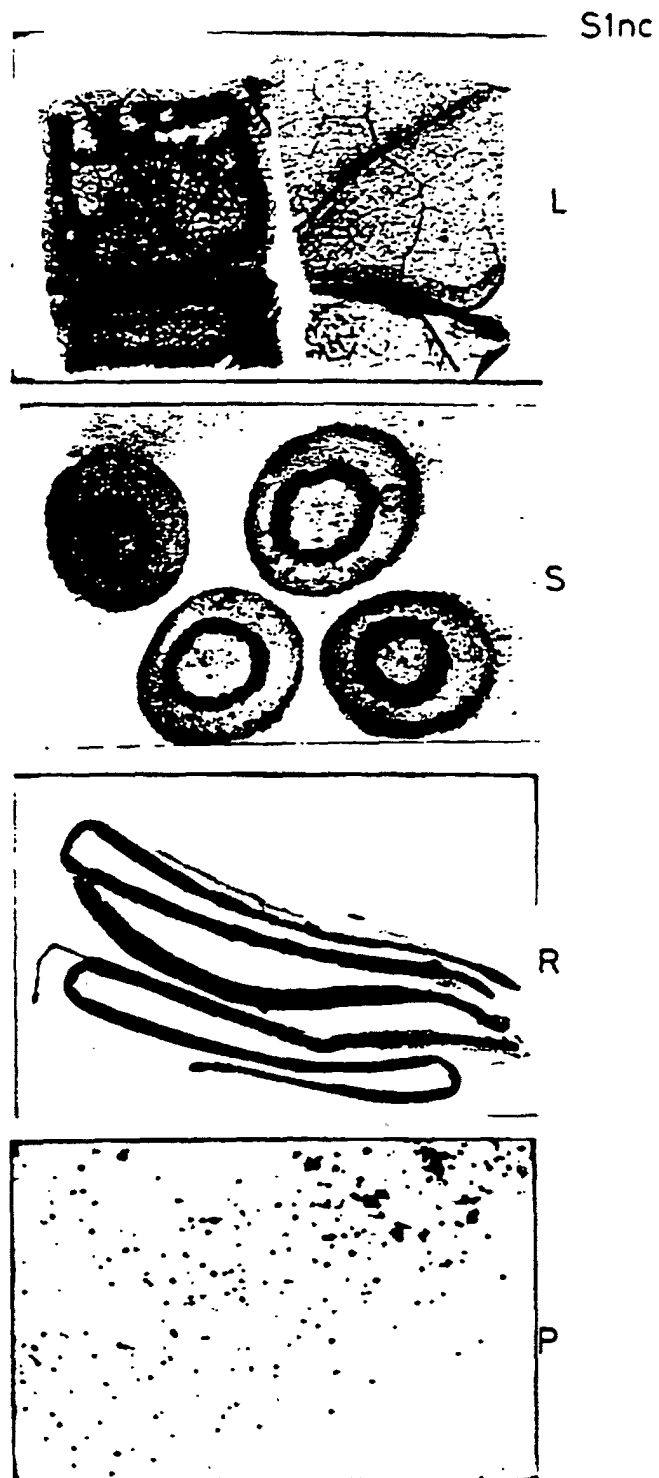


Fig. 8b

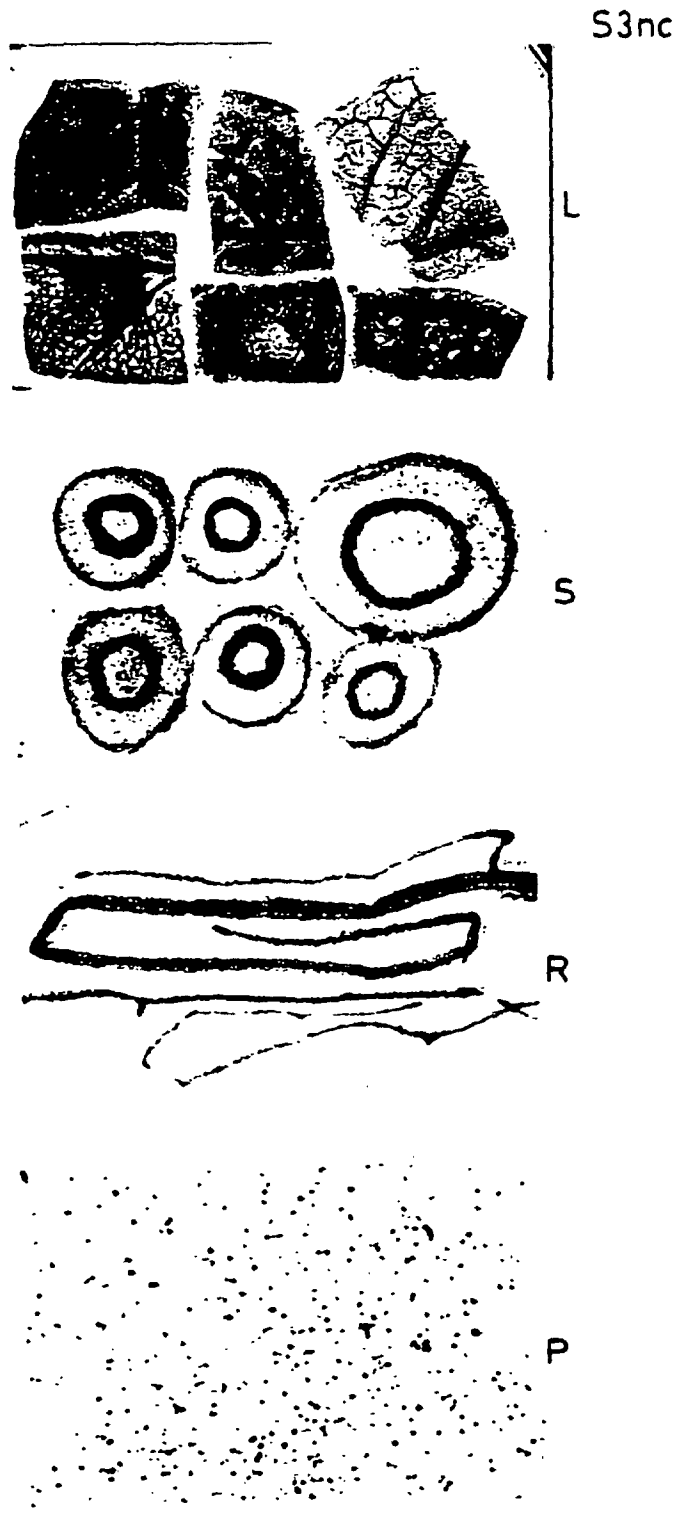


Fig. 8c

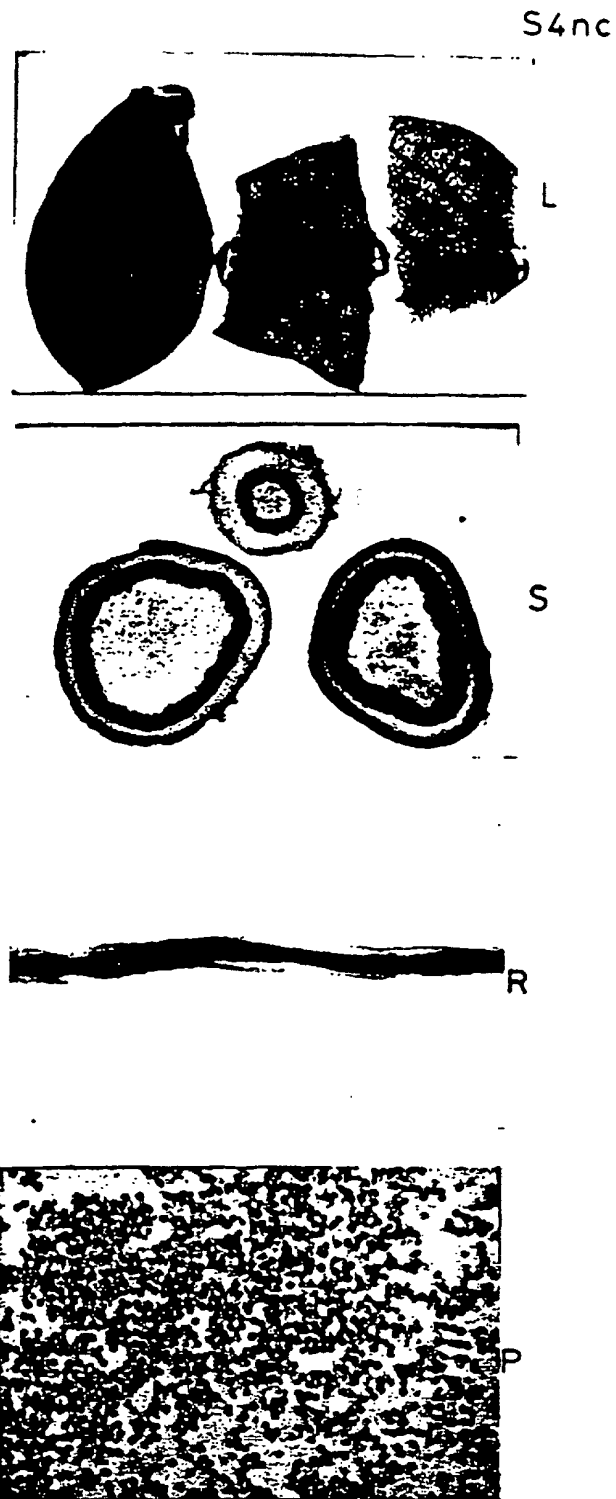


Fig. 8d

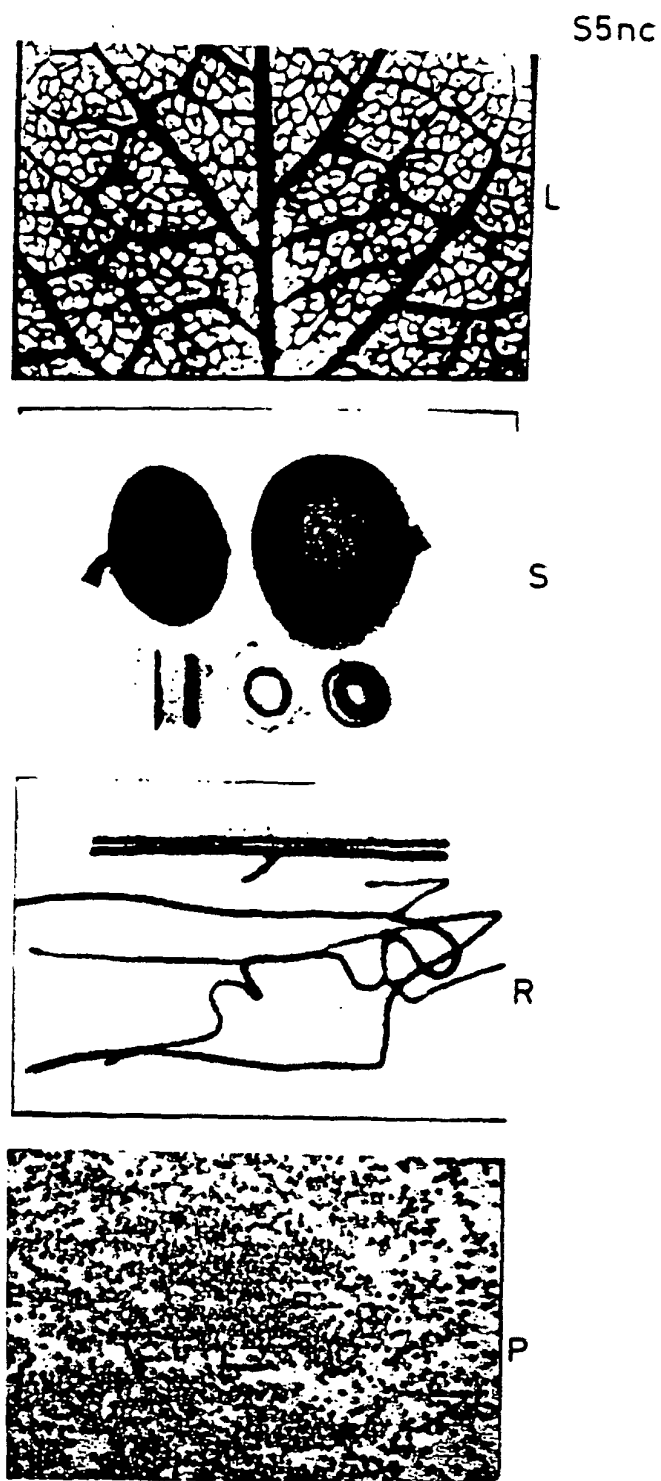


Fig. 8e

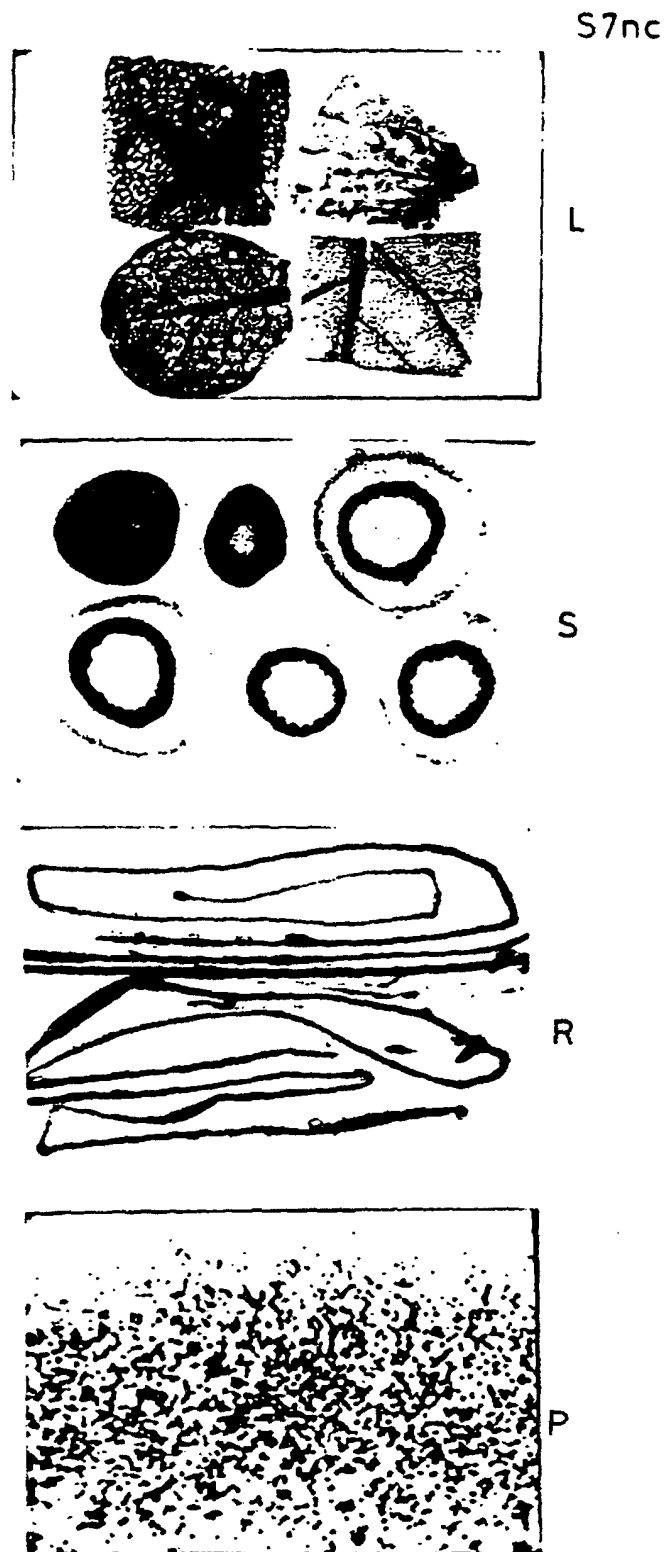


Fig. 8f

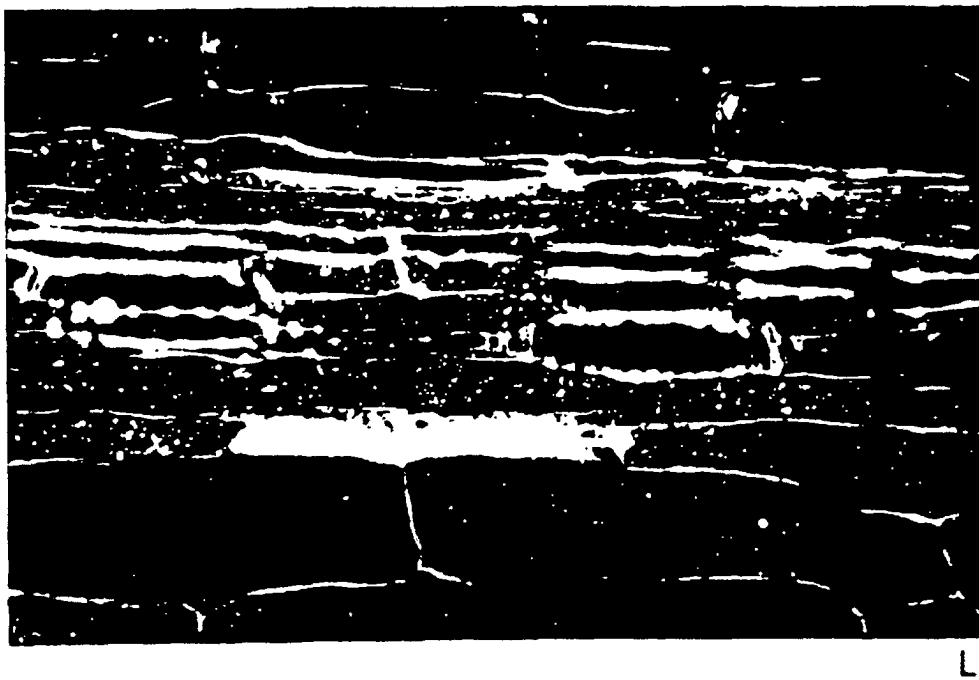


Fig. 9a

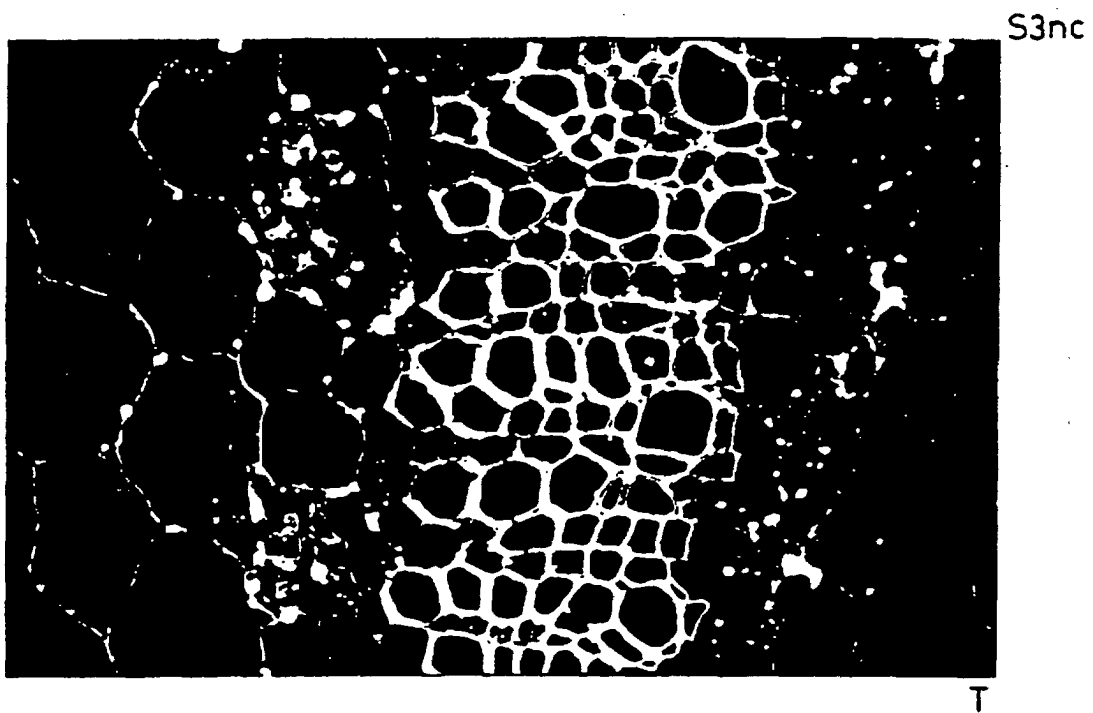
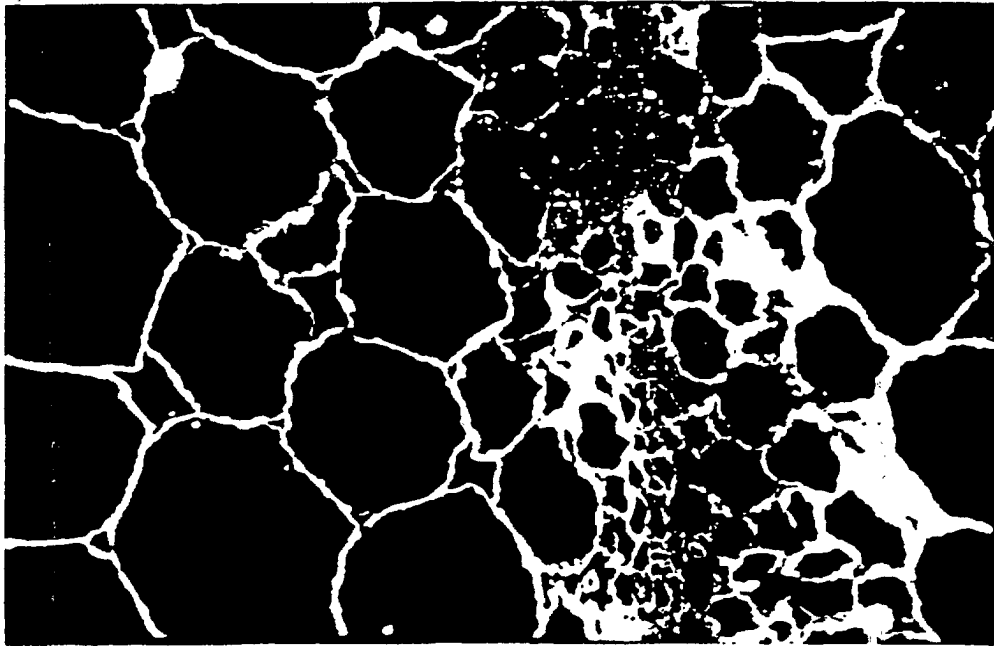
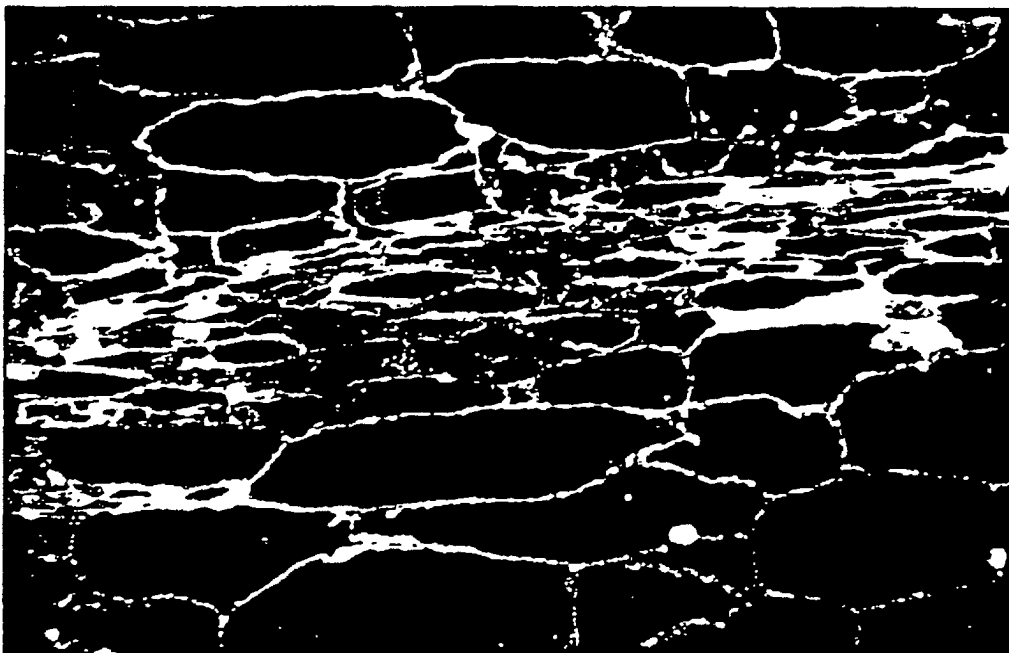


Fig. 9b

S4nc



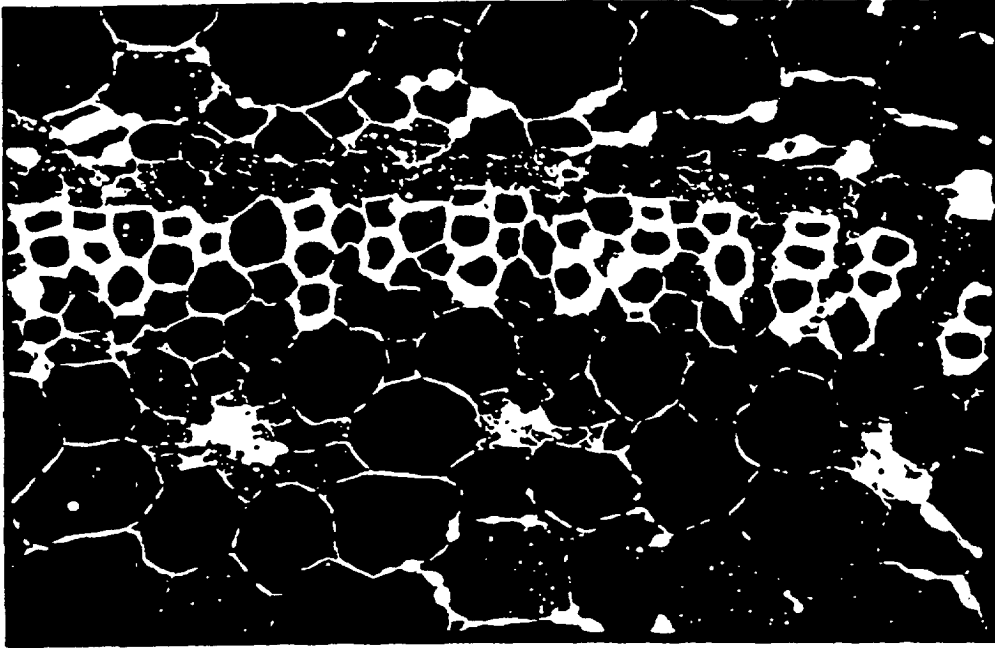
T



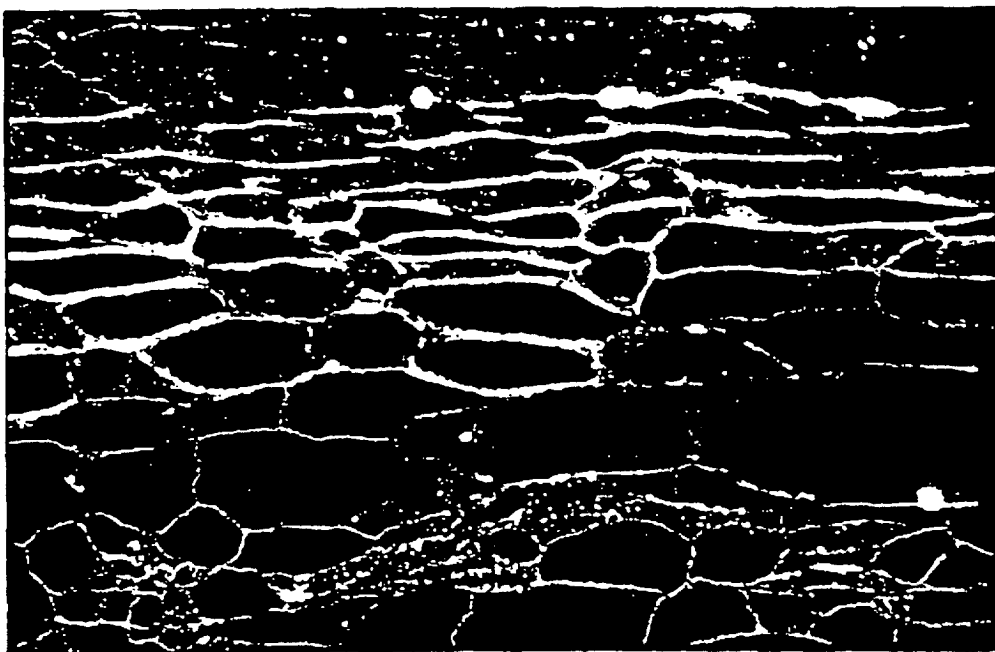
L

Fig. 9c

S5nc



T



L

Fig. 9d

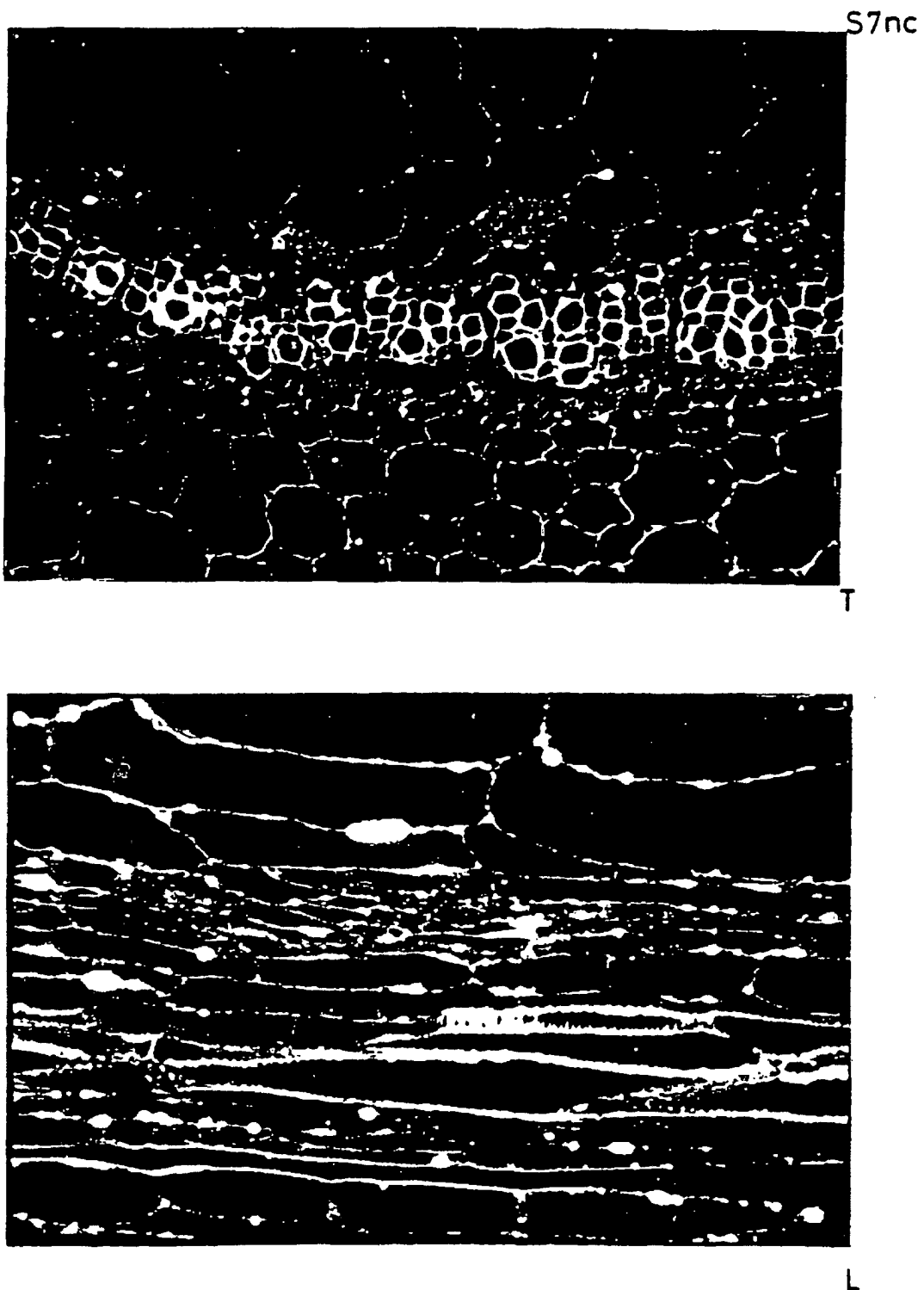


Fig. 9e

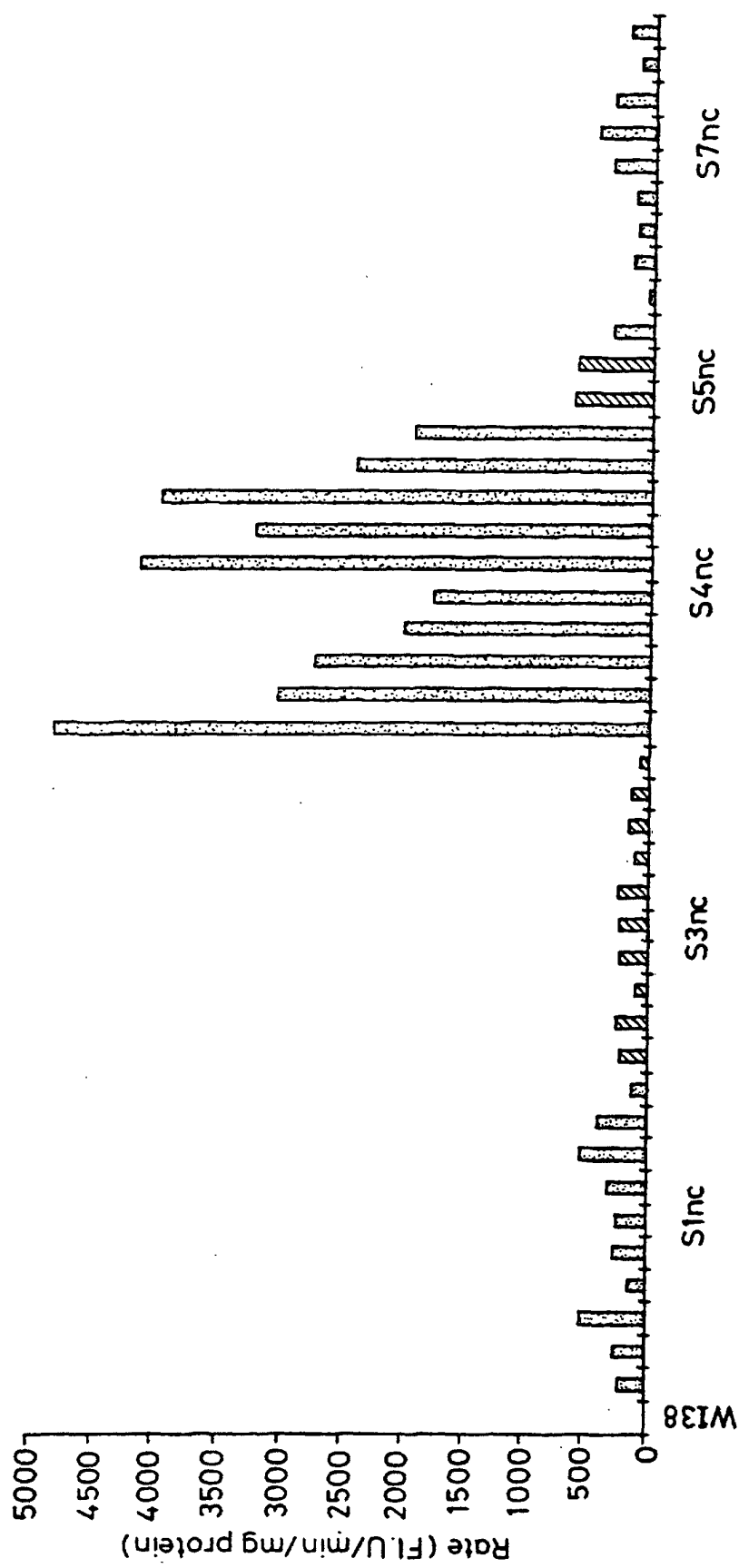


Fig.10

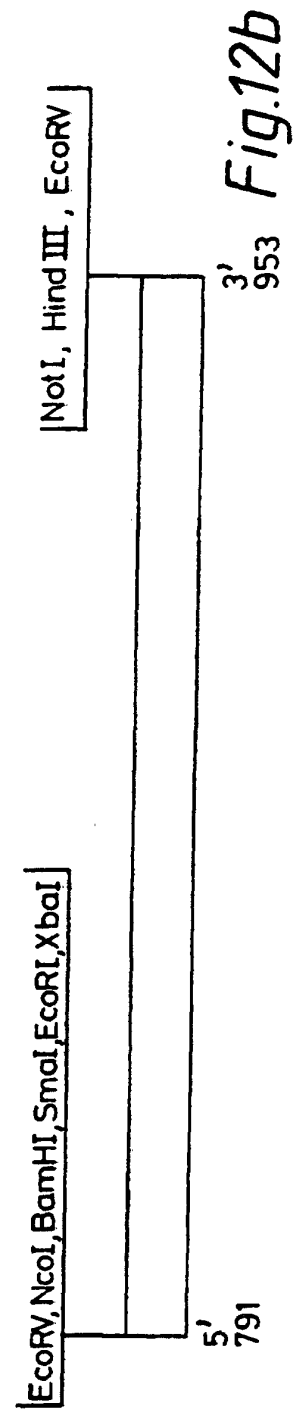
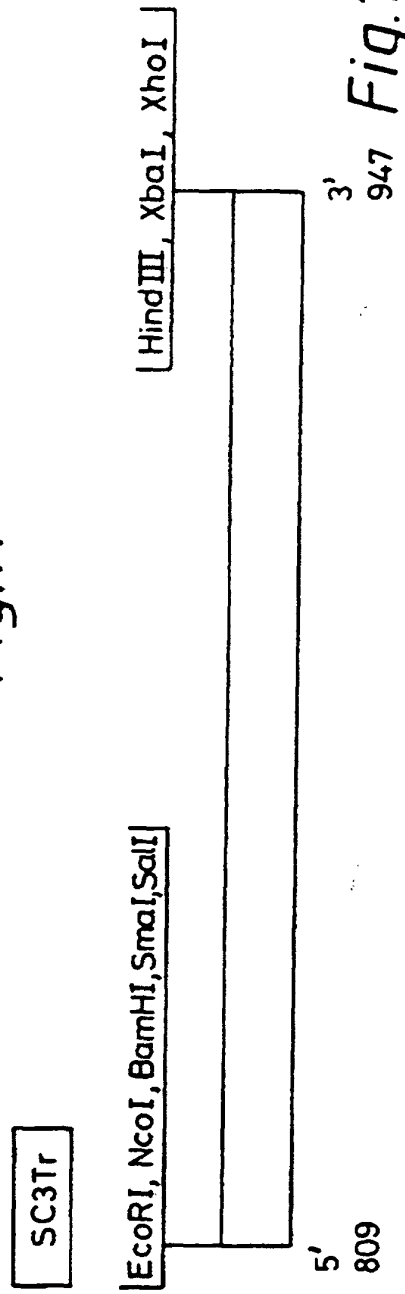
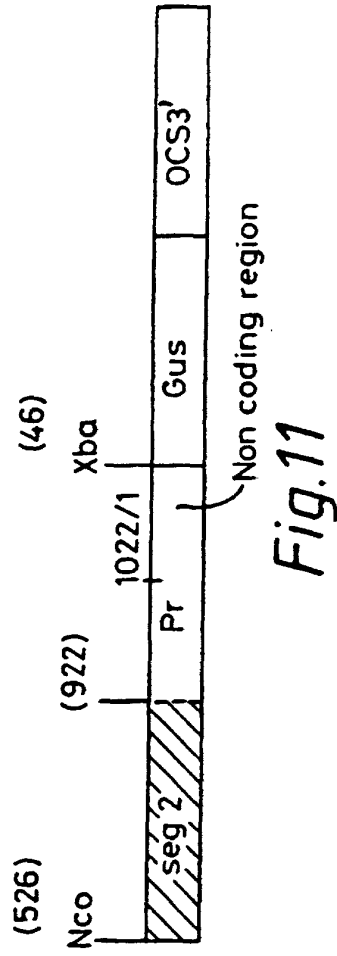




Fig.13a

Stem



Fig.13b

Leaf



Fig.13c

Stolon



Fig.13d

Tuber



Fig.14

1 TAAGTTTAGC GGGGGAAAAA GGACAGTTGA
61 ATGTTGTCAG ATGCATGTTG TAATGCTTGT
121 TGATGATGGA AACTTAAAGC TTAATACTAC
181 GGTTCTTTGT TTATCAGGAA TGCTCATTGT
241 TATTGCCCTA AATCTGGTAC TTTATCCAAA
301 TCAAGAATGA TAAACTCGTA CACTCTCTAG
361 AACCGCTTAG GAAGGAACAT ATGTGATAAG
421 AGTCGGCCCA ATTCGAGAGG ACTAGTCTCC
481 TAAACAAAAC ACATATAAAA AACCTAAAAA
541 GTGGGAACAG TTACAAATCT GCAGTCTCAC
601 CAAGTTTTCG AATGTTCTCC CACCATTCAC
661 TAGCTGACAC AACCCGTTTT GACCCAACAT
721 AATCGACTTG TCCTCAAGTC GAAAGGAGGG
781 ATTGGAGGTT GATGGATGAT TTCCTTGTGT
841 GCTTTTAATG CCTCTTGAAC TGTAGCCACA
901 AATTC

Fig. 15

TCTGTTGCTG	TTTGCAATTT	TTTAAAGGGT	60
TCATCAACAC	ATTATATGAC	TTGCAGTTGC	120
TTTTGTTTAT	TCACTTACAA	ATACCGGTTG	180
ATGTAGCTAA	AAGCTGGCCG	TTTATAGTTT	240
AACTAAATTT	GGAAACATCA	AATACTTTTT	300
GGTACTCCTG	AAATTTAAAT	CAAATCCAA	360
AACTGAAATT	TCGATTAAC	ATTACAAGAT	420
GATTACAAGG	AGTAAATATC	TTAATCTTGA	480
TATAGGAACA	TAATACATAA	ACTAAAAGTT	540
TCCCTAAATT	TGTGAGTCAC	CTTTCACCTA	600
TTTCCCTCCA	CCCGGATTCC	CTCCAATTAA	660
TGGGTTCGTA	TCAATACATC	CGGCCCGGAA	720
GAATTATTGT	GCCAAGCAAA	AAGCCATTCG	780
TTGAAAGCTT	CAAAGATCC	GGCCAAATCA	840
ACACCACTTT	GAAACCTCAA	ATCTGTTTTG	900
			905

Fig.15 (cont.)

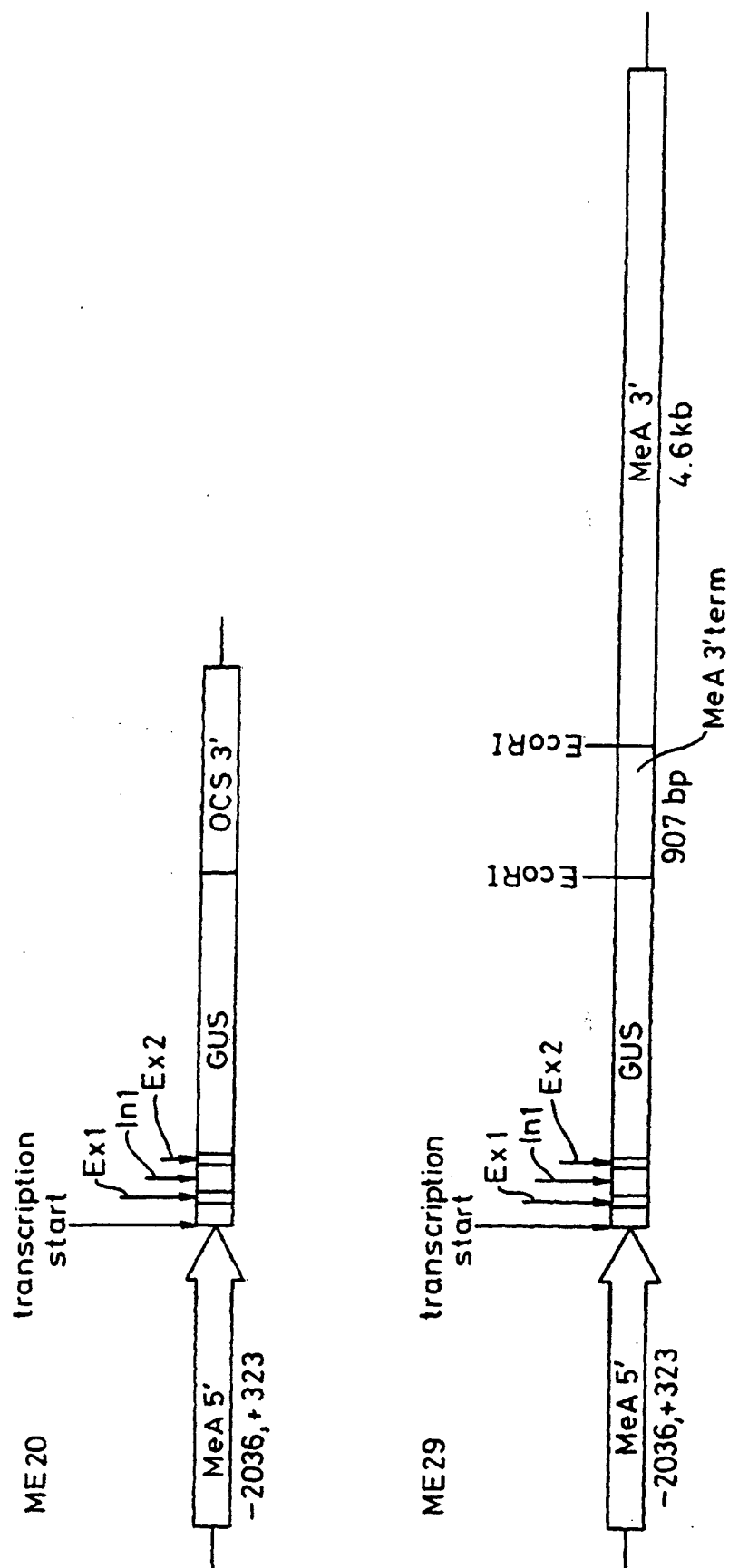


Fig. 16

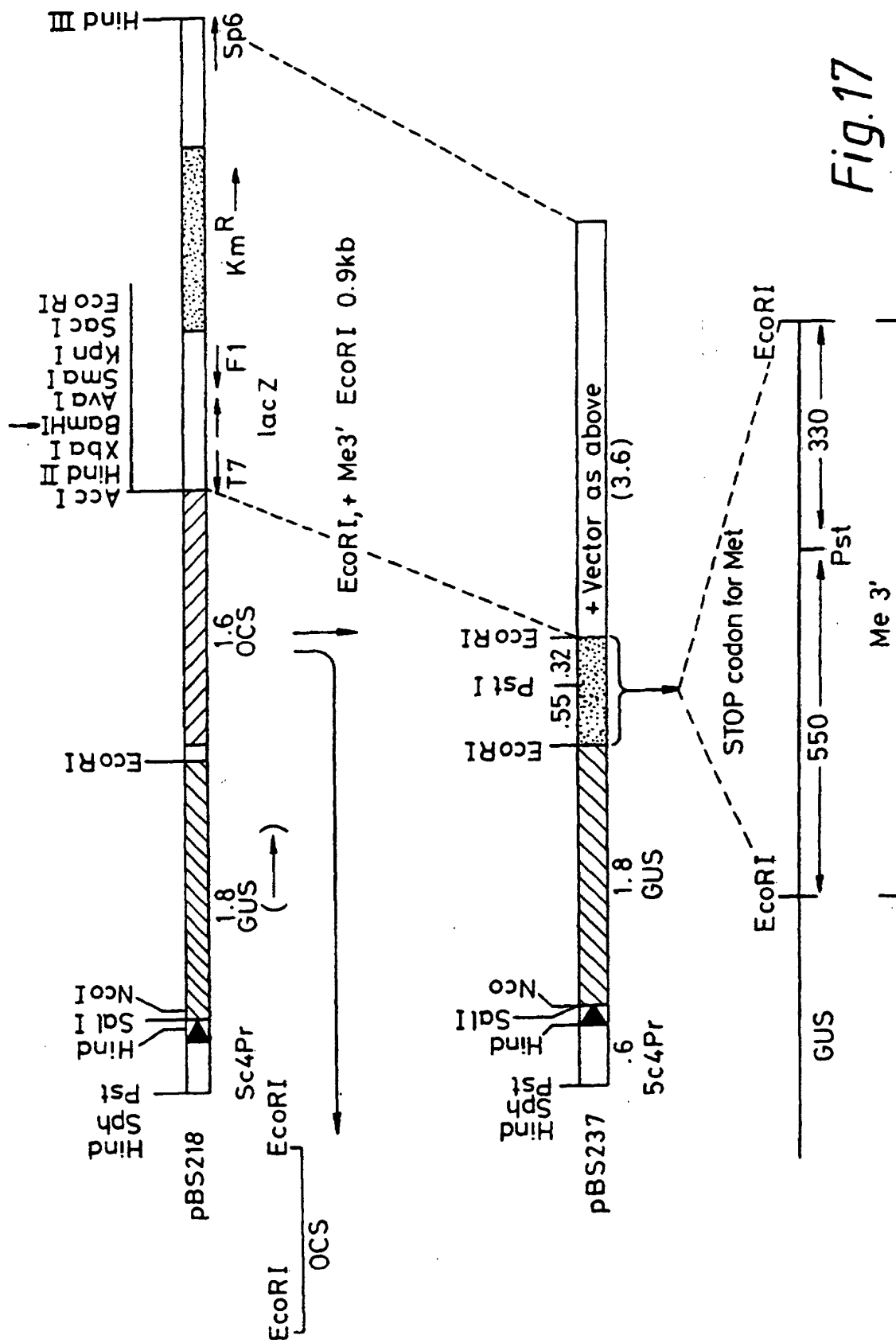


Fig.17

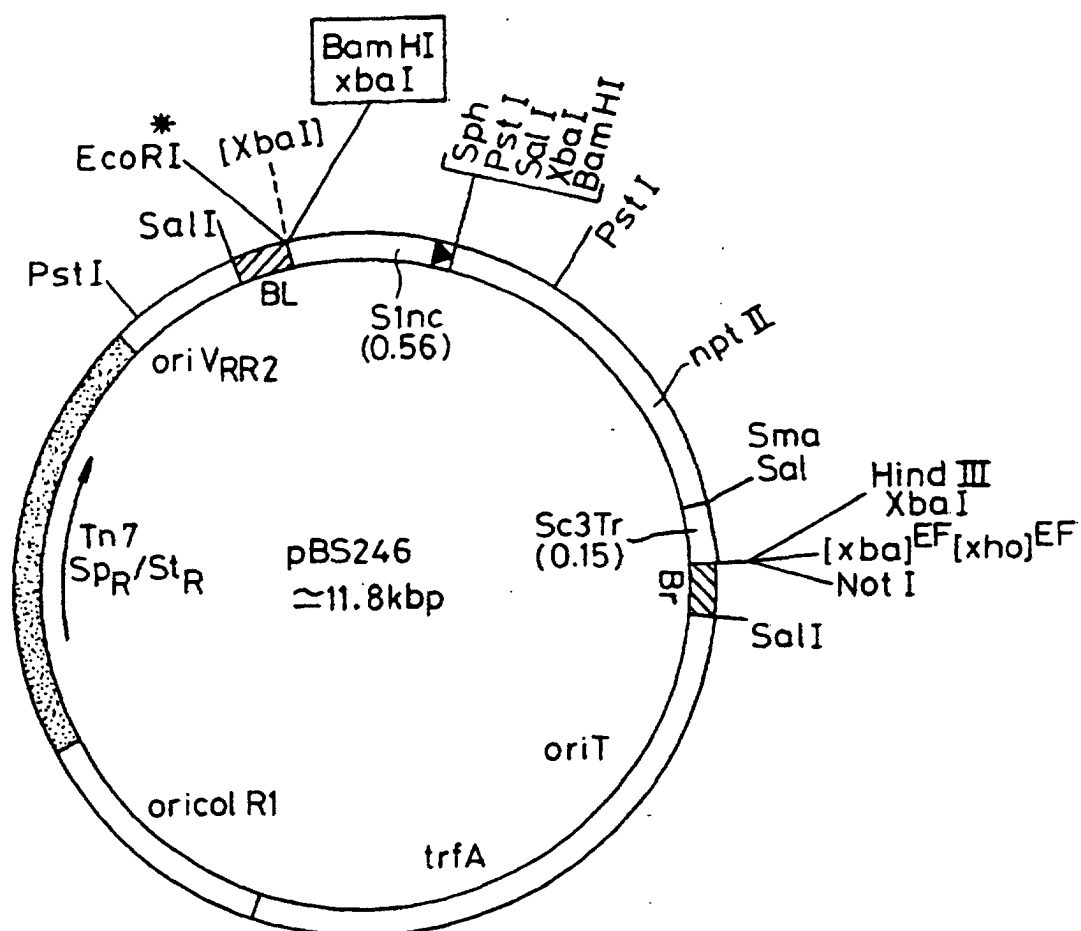
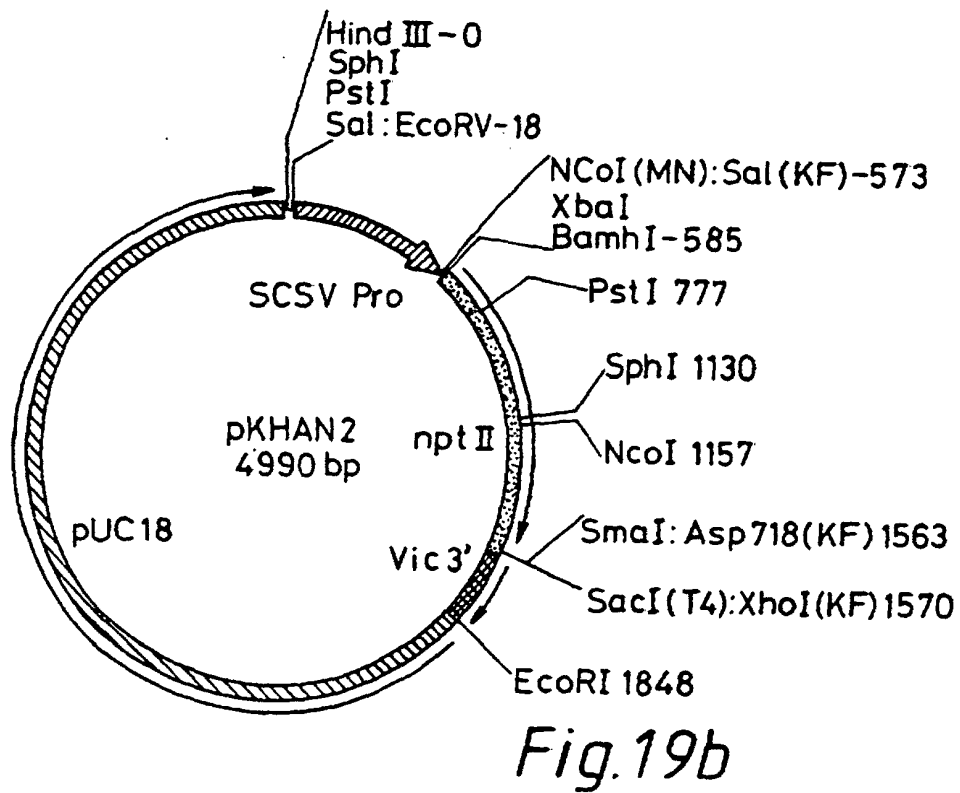
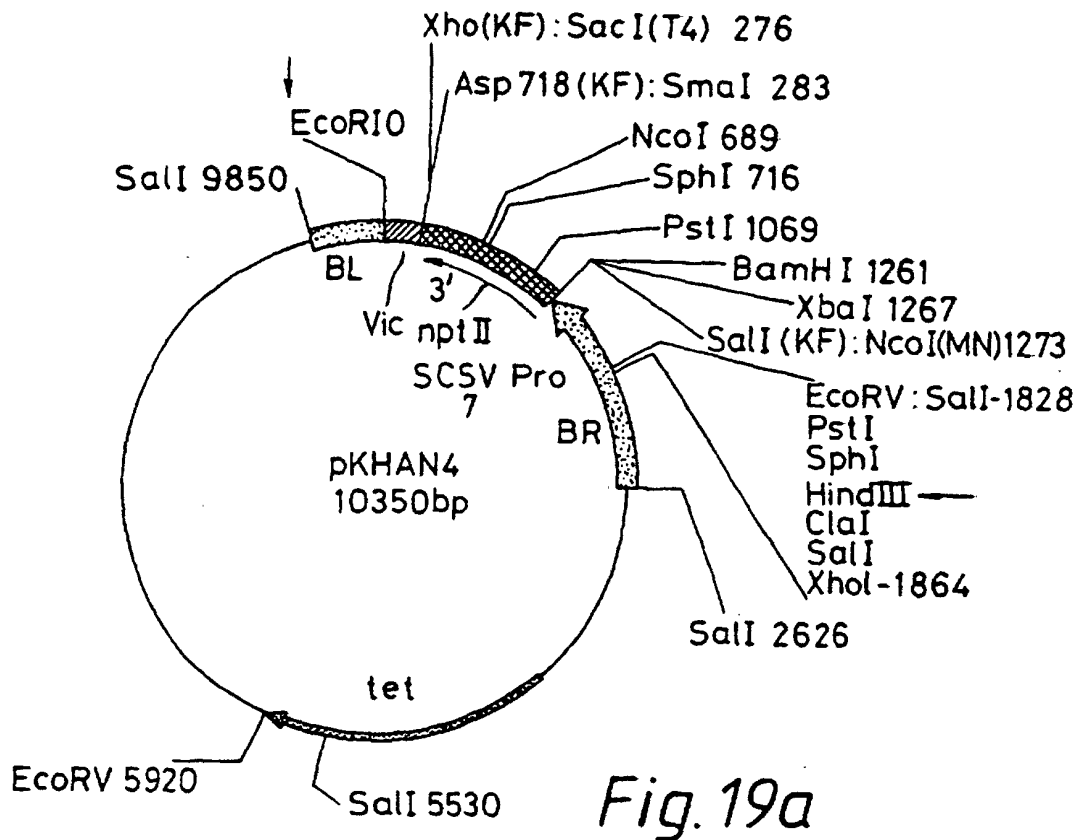


Fig. 18



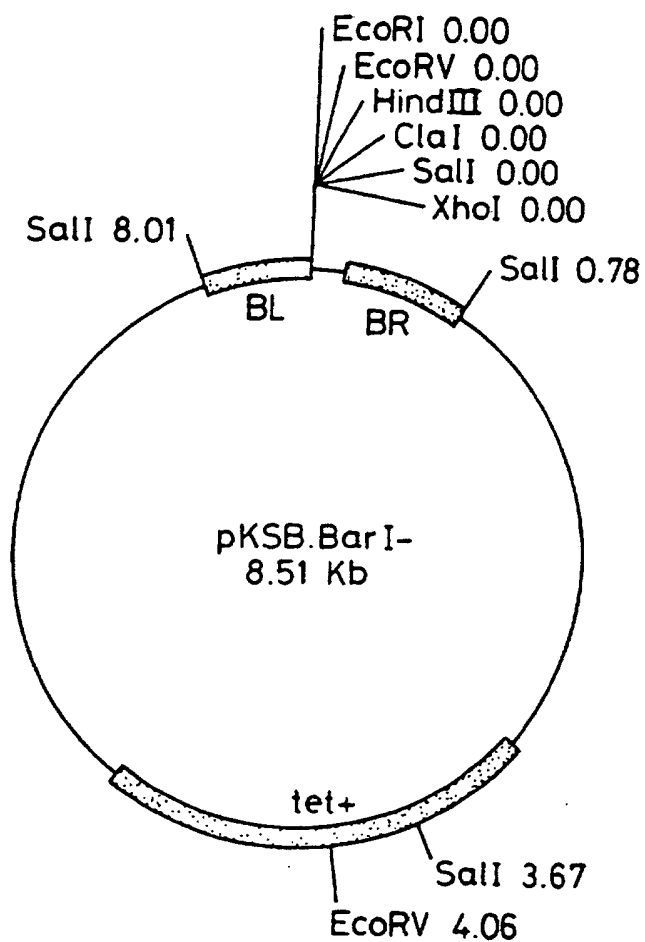


Fig. 19c

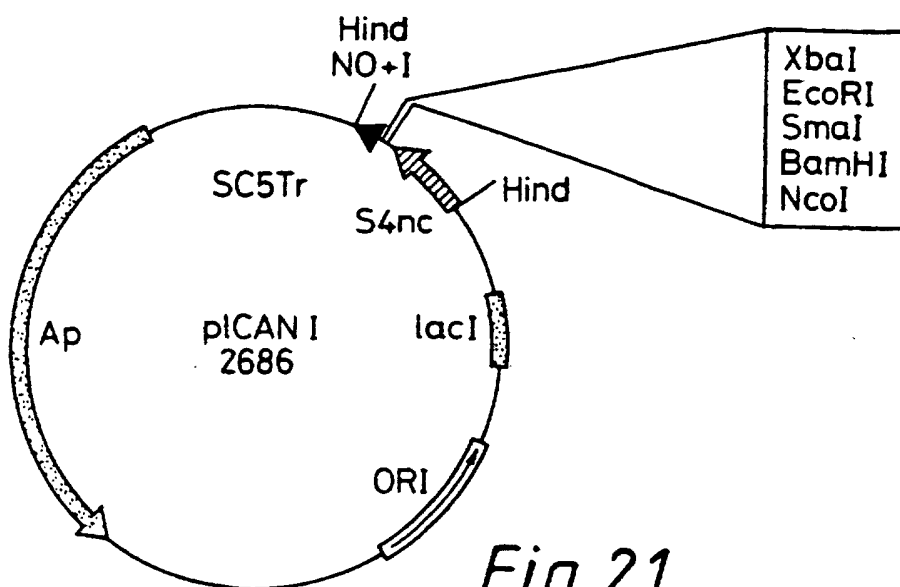


Fig. 21

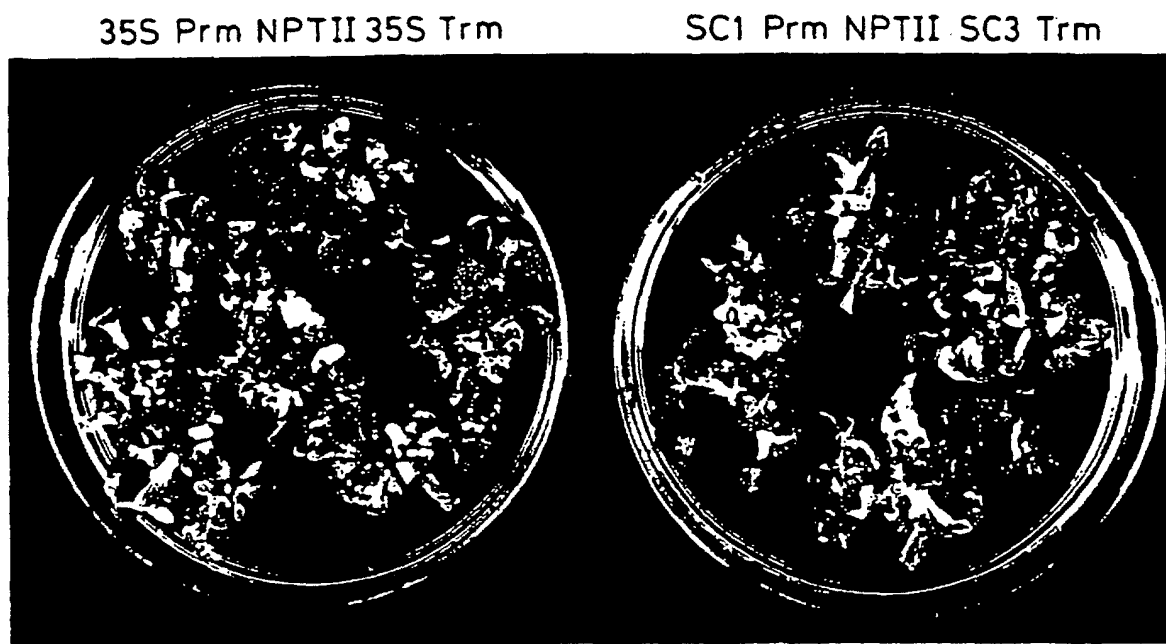


Fig. 20

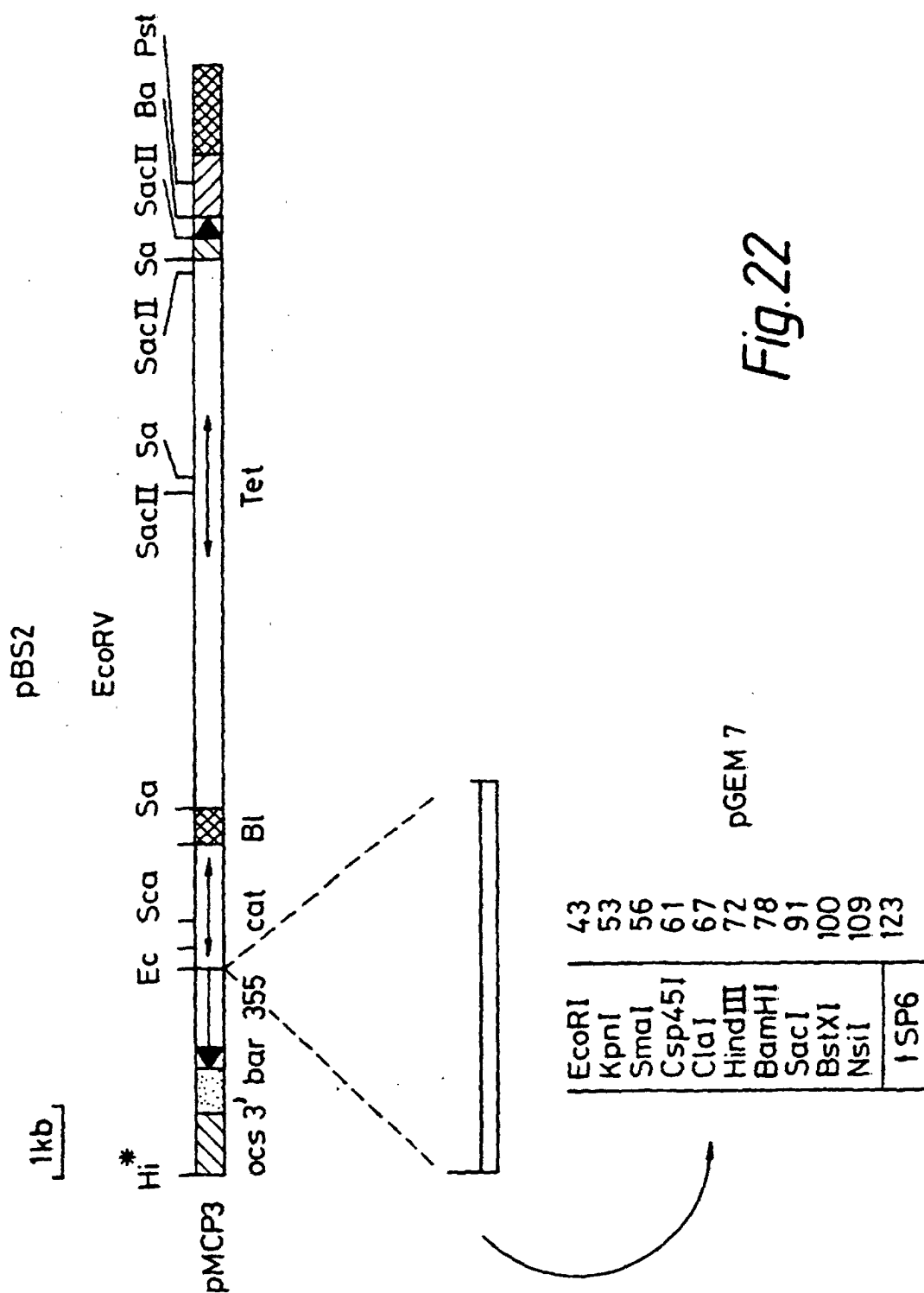


Fig.22